


```
; Sequence 2, Application US/08990379
; Patent No. 5998188
; GENERAL INFORMATION:
; APPLICANT: Stork, Philip J
; APPLICANT: Misra-Press, Anita
; TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
; FILE REFERENCE: 4104-000322USA
; CURRENT APPLICATION NUMBER: US/08/990,379
; CURRENT FILING DATE: 1997-12-15
; EARLIER APPLICATION NUMBER: PCT/US96/10402
; EARLIER FILING DATE: 1996-06-14
; EARLIER APPLICATION NUMBER: 60/000,263
; EARLIER FILING DATE: 1995-06-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1993
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-08-990-379-2

Query Match          5.6%; Score 48.6; DB 2; Length 1993;
Best Local Similarity 50.6%; Pred. No. 3.9e-05;
Matches 117; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Qy 231 ttcaagaagaatttaattcaattcaacagatgcccggctccgggtggaagctgctgtga 290
    ||||| ||| || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1155 ttcatggaagccatcgaatacatagacgagtgagagctgcgagggcgagctgtcgtt 1214

Qy 291 cactgcctgcgggggtccacagagcgtgacactgtgtgcatcatcatatgacgctc 350
    ||||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1215 cactgcggcgccatctcagatcagccacatctgcctgcctgaactgagtatgaag 1274

Qy 351 actgaactgtgctggagatgacatgcacacgctgcgctggcgagagatcctgtgcaac 410
    ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1275 aaacgggagagcgtgagagagcttcgagctgcgtcaagcagcgctgagatcatctgc 1334

Qy 411 cccaacgtggctccagagacagctccagagatttgagaagcatgagctc 461
    ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1335 cccaactcagctcatgtgagccagttgctgagctcagctcagctc 1385

RESULT 5
US-09-045-973-6
; Sequence 6, Application US/09045973
; Patent No. 6165767
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: PROTEIN PHOSPHATASE RELATED MOLECULES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,973
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0491 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1729 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT16
CLONE: 3041794
US-09-045-973-6

Query Match          5.5%; Score 47.8; DB 4; Length 1729;
Best Local Similarity 55.0%; Pred. No. 6.4e-05;
Matches 94; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 284 cctgtacactgctgcgggggtctccagagagctgacactgtgtatcgtatcatcat 343
    ||| ||||| ||||| ||| ||| ||| ||| ||| ||||| ||||| ||||| ||||| |||
Db 812 CTGTGTGACACTGTGCTGAGGGGTGAGCGCTCAGCCACGCTGTATCGGTACCTGAT 871

Qy 344 gaccgtcactgacttggctggagagatgacctgcacacgctgcgtgcggagagatcctg 403
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 872 GAAATTCACAAACGTCCTGTCGAGGCGTACAACTGGGTGAAAGCCCGGCACTGT 931

Qy 404 tgcacaccacagctggctccagagacagctccagagatttgagaagca 454
    || ||||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 932 CATCAGGCCCAACGTAGGCTTCTGTGAGGCAACTGATAGACGACGCCCA 982

RESULT 6
US-09-163-833-3
; Sequence 3, Application US/09163833
; Patent No. 6268135
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NO. 6268135el Phospholipase Molecule and Uses Therefor
; FILE REFERENCE: nm1-059
; CURRENT APPLICATION NUMBER: US/09/163,833
; CURRENT FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(594)
; US-09-163-833-3

Query Match          4.3%; Score 38; DB 4; Length 594;
Best Local Similarity 53.0%; Pred. No. 0.038;
Matches 105; Conservative 0; Mismatches 90; Indels 3; Gaps 1;

Qy 280 gctgcctgtacactgctgcgggggtctccagagagctgacactgtgtatcgtatcata 339
    || ||||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 398 gctgtcgtgtacactgtgccatggtggtgaagcgcgtctgcgcaactgttctgtgcttcc 457

Qy 340 tcatgacgctacactgtgtgtggtgagatgacctgcacacgctgcgtgcggagagat 399
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 458 tcatgtatatagagacatgacgctgtgtagagcattccagacggtgtagcgccacg-- 515
```


STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0470 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MUSCNOT02
CLONE: 971204
US-09-013-881-12

OTHER INFORMATION: Xaa = any amino acid

OTHER INFORMATION: Add = ally amino acids

```

; FEATURE:
; NAME/KEY: misc_feature

```

```

: LOCATION: (589)..(591)
: OTHER INFORMATION: Xaa = any amino acid
:
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (592)..(594)
: OTHER INFORMATION: Xaa = any amino acid
US-09-164-193-7

```

Query Match	3.9%	Score 34	DB 4	Length 814
Best Local Similarity	53.8%	Pred. No. 0.78		
Matches 70; Conservative	0;	Mismatches 60;	Indels 0;	Gaps 0;

[illegible]

RESULT 14

US-08-232-463-14/c
; Sequence 14, Application US/08232463

```

: GENERAL INFORMATION:
: APPLICANT: DORNER, F.
: APPLICANT: SCHEIFLINGER, F.
: APPLICANT: FALKNER, F. G.
: TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
: NUMBER OF SEQUENCES: 52

```

```

1 ZIP: 22313-0299
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: Floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: PatentIn Release #1.0, Version #1.25
12
13 CURRENT APPLICATION DATA:

```

```

? INFORMATION FOR SEQ ID NO: 14:
? =====
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 7218 base pairs
?     TYPE: nucleic acid
?     STRANDEDNESS: single
?     TOPOLOGY: linear
?     IMMEDIATE SOURCE:
?     CLONE: pTZ9pt-P15

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US-08-232-463-14

Query Match	3.98;	Score	34;	DB	1;	Length	7218;
Best Local Similarity	12.2%;	Pred. No.	2.8;				
Matches	46;	Conservative	156;	Mismatches	176;	Indels	0;
						Gaps	0;

QY	427	aagaacgcctccaaagatttggaagaataggatcagtactgagtcgtcgaaag	486
Db	1340	RR	1283
QY	487	aagaatacggagagagcccttgcagatgcagaagaaccaaaacattcgcgcctc	546
Db	1280	RR	1223
QY	547	caggaattcgaagttctggccttctcagaagactgttaagtacctgaattctgaa	606
Db	1220	RR	1163
QY	607	atatgcaaaccccaaagtttagtcgtcgtcgccaagaagaagacaalagatt	666
Db	1160	RR	1103
QY	667	aagatccagtagyattttaactgtttcatctgaagtgaatalatacyagtc	726
Db	1100	RR	1043
QY	727	atgttatgttgagaactaagabatatctttagcaagaagaanaatatltcccattcc	786
Db	1040	AAGCTCGGAATTAATTCTGTGAGCGTATGSCAACAAGAAMAATAATTATAGTCGG	981
QY	787	cactgcgtggaagttc	804
Db	980	CACCTCATGGGCATTTTC	963

RESULT 15

PCT-US95-14418-1
; Sequence 1, Application PC/TUS9514418

APPLICANT :
APPLICANT :
TITLE OF INVENTION: DNA Encoding a Thermostable DNA Polymerase Enzyme
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois

```

1      COMPUTER READABLE FORM:
2      MEDIUM TYPE: Floppy disk
3      COMPUTER: IBM PC compatible
4      OPERATING SYSTEM: PC-DOS/MS-DOS
5      SOFTWARE: PatentIn Release #1.0, Version #1.25
6      CURRENT APPLICATION DATA:

```

1 CLASSIFICATION:
2
3 ATTORNEY/AGENT INFORMATION:
4
5 NAME: Gass, David A.
6
7 REGISTRATION NUMBER: 38,153
8
9 REFERENCE/DOCKET NUMBER: 28003/32330
10
11 TELECOMMUNICATION INFORMATION:
12

```

; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3048 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2002, 16:09:41 ; Search time 23.37 Seconds

(without alignments)
529.321 Million cell updates/sec

Title: US-09-544-525-2

Perfect score: 897
Sequence: 1 MGNMKNKILPGIYGNFKDA.....AKNIIAAPGILKFWAFRLRL 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_1101:*

1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT:*
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7: /SIDSR/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDSR/gcgdata/geneseq/geneseq/AA1987.DAT:*
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14: /SIDSR/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDSR/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDSR/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDSR/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDSR/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDSR/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	891	99.3	167	AA823298	Human dual-specific
2	831.5	92.7	184	AA568795	Amino acid sequenc
3	831.5	92.7	184	AA873216	Human phosphatase
4	831.5	92.7	184	AA873217	Human dual-specific
5	831.5	92.7	184	AA864321	Human DSP-3 protei
6	791.5	88.2	184	AA873213	Murine phosphatase
7	753.5	84.0	205	AA881105	Human JNK activati
8	715.5	79.8	205	AA866443	Murine JNK-3 varia
9	702.5	78.3	205	AA881106	Murine DSP-3 activ
10	644	71.8	145	AA866442	Human MAP-kinase p
11	458.5	51.1	329	AA864840	Human SGP008 phosph

12	433.5	48.3	96	AA841570
13	210	23.4	482	AA829641
14	210	23.4	482	AA818655
15	210	23.4	482	AA873225
16	209	23.3	218	AA873217
17	207	23.1	179	AA825664
18	207	23.1	341	AA873226
19	207	23.1	659	AA820331
20	205	22.9	157	AA810274
21	205	22.9	157	AA806779
22	203.5	22.7	170	AA806780
23	203.5	22.7	170	AA866436
24	203.5	22.7	663	AA829150
25	197	22.0	168	AA806778
26	197	22.0	168	AA866435
27	196	21.9	170	AA806777
28	196	21.9	170	AA866434
29	196	21.9	189	AA853302
30	191	21.3	170	AA806785
31	191	21.3	552	AA806772
32	191	21.3	552	AA807042
33	191	21.3	1049	AA804833
34	187	20.8	661	AA844927
35	186.5	20.8	665	AA804834
36	186.5	20.8	666	AA820325
37	186.5	20.8	672	AA825784
38	186	20.7	171	AA806784
39	186	20.7	171	AA866440
40	185	20.6	221	AA818667
41	183.5	20.5	223	AA839734
42	183.5	20.5	236	AA841520
43	181	20.2	552	AA807043
44	175	19.5	220	AA873215
45	175	19.5	784	AA844923

ALIGNMENTS

RESULT 1	
AA823298	standard; Protein: 167 AA.
ID	AA823298
XX	
AC	AA823298;
XX	
DT	09-FEB-2001 (first entry)
XX	
DE	Human dual-specificity MAP kinase phosphatase DSP-3.
XX	
KW	Human DSP-3; dual-specificity phosphatase; antibody;
KW	dual-specificity MAP kinase phosphatase family; PTP; recombinant production;
KW	protein tyrosine phosphatase family; PTP; recombinant production;
KW	proliferative response; cell differentiation; cell survival;
KW	proliferative disorder; cell cycle abnormality; metabolic disease;
KW	Duchenne muscular dystrophy; cancer; graft-versus-host disease;
KW	autoimmune disease; allergy.
XX	
OS	Homo sapiens.
XX	
PN	W0200060092-A2.
XX	
PD	12-OCT-2000.
XX	
PE	07-APR-2000; 2000WO-US09185.
XX	
PR	07-APR-1999; 99US-0128225.
XX	
PR	02-JUL-1999; 99US-0142338.
XX	
PA	(CEPT-) CEPTYR INC.
XX	
PI	Luchoe RM, Wei B;
XX	
DR	WPI: 2000-665011/64.

Human ORFX ORF1334
Human dual-specific
A human regulator
Human phosphatase
Murine phosphatase
Human protein sequ
Human phosphatase
Human protein phos
Arabidopsis thalia
Human dual-specific
Human MAP-kinase p
Dual-specific mur
Human dual-specific
Human MAP-kinase p
Human dual-specific
Human MAP-kinase p
Human colon cancer
Human dual-specific
Human dual-specific
Human dual-specific
Human SGP006 phosph
Zea mays MAP kinas
Human SGP002 phosph
Human protein phosph
Human protein sequ
Human dual-specific
Human MAP-kinase p
A human regulator
Human polypeptide
Human dual-specific
Murine phosphatase
A. thaliana MAP Ki

DR N-PSDB; AAC63800.

XX Novel dual-specificity mitogen activated protein kinase phosphatase
PT polypeptide useful in screening assays for identifying agents that
PT modulate activity of the protein which are useful for treating cancer
PT and autoimmune diseases

PS Claim 1; Fig 2; 60pp; English.

XX The invention relates to a human dual-specificity mitogen-activated
CC protein (MAP) kinase phosphatase, DSP-3, and to nucleic acids encoding
CC it. The invention also relates to variants of DSP-3 which retain
CC activity, expression vectors and host cells comprising DSP-3 encoding
CC DNA, the recombinant production of DSP-3, an anti-DSP-3 antibody, and
CC a DSP-3 substrate-trapping mutant protein that has a reduced ability to
CC phosphorylate a substrate relative to the wild-type DSP-3. The
CC invention additionally encompasses use of a DSP-3 modulator to modulate
CC a proliferative response, cell differentiation or cell survival. The
CC DSP-3 protein is useful for screening an agent that binds to DSP-3 and/or
CC modulates DSP-3 activity, and is also useful for raising antibodies. DNA
CC encoding DSP-3 or a reporter protein is also useful for screening an
CC agent that modulates DSP-3 activity. The identified agents that
CC modulate DSP-3 activity are useful for treating Duchenne muscular
CC dystrophy, cancer, graft-versus-host disease, autoimmune diseases,
CC allergies, metabolic diseases, abnormal cell growth, abnormal cell
CC proliferation and cell cycle abnormalities. DSP-3-specific antibodies
CC and DSP-3 antisense probes are useful for detecting DSP-3 expression in
CC a sample. The present sequence represents human DSP-3.

XX Sequence 167 AA:

Query Match 99.3%; Score 891; DB 21; Length 167;
Best Local Similarity 99.4%; Pred. No. 3.9e-101;

Matches 166; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MGNGMKNKILPGLYIGNFKDARDAEOLSKNKVTHILSVHDSPLCWRTRHFKESIKFIHEC 60
DB 1 mgngmknkllpglyignfkardaeqlsknkvhilsvhdsplcwrtrfhkesikfihc 60
OY 61 RRGSCVHCHAGVSRSVTIVAYIMVTDFGWDALHTVAGSCANPNVGFQROLOE 120
DB 61 rrgscvchclagvsrsvtlvayimvtldfgwedahtvagscannpvgfqrqlqe 120
OY 121 FEKHEVHOYROWLKEEYGESPLQDAEAKNIAPGILKFWAFILRL 167
DB 121 fekehvhyrgwlkeeygesplqdaeeakniapgilkwafilrll 167

RESULT 2

AAV68795 AAY68795 standard; Protein; 184 AA.

XX AAY68795;

DT 16-MAY-2000 (first entry)

XX Amino acid sequence of a human phosphorylation effector PHSP-27.

XX Human; phosphorylation effector; PHSP; proliferative disorder;

KW Immune disorder; neuronal disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 36 /note= "potential phosphorylation domain"

FT Modified-site 40 /note= "potential phosphorylation domain"

FT Modified-site 50 /note= "potential phosphorylation domain"

FT Modified-site 62 /note= "potential phosphorylation domain"

FT Modified-site /note= "potential glycosylation domain"

FT

FT Domain 63..118 /note= "tyrosine phosphatase active site domain"

FT Modified-site 70 /note= "potential phosphorylation domain"

FT Modified-site 105 /note= "potential phosphorylation domain"

FT Modified-site 117 /note= "potential phosphorylation domain"

FT Modified-site /note= "potential phosphorylation domain"

XX WO200006728-A2.

XX 10-FEB-2000.

XX 28-JUL-1999; 99WO-0517132.

XX 28-JUL-1998; 98US-0123494.

XX 14-SEP-1998; 98US-0152814.

XX 14-OCT-1998; 98US-0173482.

XX 03-NOV-1998; 98US-0106889.

XX 19-NOV-1998; 98US-0109093.

XX 22-DEC-1998; 98US-0113796.

XX 12-JAN-1999; 98US-0173482.

XX 12-JAN-1999; 99US-0229005.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;

XX Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzal Y;

XX Reddy R, Lu DAM, Shih LL;

XX WPI; 2000-183125/16.

XX N-PSDB; AA246164.

XX New human phosphorylation effectors useful for the diagnosis, treatment

XX and prevention of proliferative, immune and neuronal disorders

XX Claim 1; Page 114-115; 142pp; English.

XX AAY68795 and AAY68797-99 represent human phosphorylation effectors

XX (PHSP), designated PHSP1-PHSP3 (the protein sequence for PHSP2 is not

XX given in the specification). The sequences were isolated from cDNA

XX libraries prepared from various human tissues. The PHSP proteins are

XX useful for the diagnosis, treatment and prevention of proliferative

XX disorders, immune disorders and neuronal disorders. The PHSP proteins

XX form pharmaceutical compositions which useful for treating or preventing

XX disorders associated with decreased PHSP expression/activity. PHSP

XX antagonists are useful for treating or preventing disorders associated

XX with increased PHSP expression/activity.

XX Sequence 184 AA;

Query Match 92.7%; Score 831.5; DB 21; Length 184;

Best Local Similarity 88.6%; Pred. No. 9e-94;

Matches 163; Conservative 0; Mismatches 4; Indels 17; Gaps 2;

OY 1 MGNGMKNKILPGLYIGNFKDARDAEOLSKNKVTHILSVHDSPLCWRTRHFKESIKFIHEC 45

DB 1 mgngmknkllpglyignfkardaeqlsknkvhilsvhdsarpmlegvkvylcipadps 60

OY 46 --RTRHFKESIKFIHECRLGSCVHCHAGVSRSVTIVAYIMVTDFGWDALHTVRA 103

DB 61 qnltrfhkesikfihcrlrgescvchclagvsrsvtlvayimvtldfgwedahtvra 120

OY 104 GRSCANPNVGFQROLOEFKHEVHOYROWLKEEYGESPLQDAEAKNIAPGILKFWAF 163

DB 121 grscanpvnvgfqrqlqefekhvhoyrowlkeeygesplqdaeeakniapgilkwaf 180

OY 164 LRRL 167

DB 181 lrll 184

```
RESULT 3
AAB73216
ID AAB73216 standard; Protein; 184 AA.
XX
AC AAB73216;
XX
DT 11-MAY-2001 (first entry)
XX
DE Human phosphatase AAB74753_h.
XX
KW Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia;
KW cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia;
KW congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease;
KW Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;
KW schizophrenia; hamartoma.
XX
OS Homo sapiens.
XX
PN WO200112819-A2.
XX
PD 22-FEB-2001.
XX
PE 11-AUG-2000; 2000WO-US22158.
XX
PR 13-AUG-1999; 99US-0149005.
XX
PA (SUGEN-) SUGEN INC.
XX
PI PLOWMAN GD, MARTINEZ R, WHYTE D, HILL R, FLANAGAN P, LIJOUNIN M;
XX
DR WPI; 2001-211226/21.
XX
DR N-PSDB; AAF63568.
XX
XX
PT New protein phosphatase polypeptide for diagnosing and treating
PT phosphatase related disorders such as cancer, schizophrenia, cardiac
PT dysfunction and/or vascular disorders
XX
PS Claim 6; Fig 5; 138pp; English.
XX
CC The present invention relates to phosphatase proteins and coding
CC sequences. The present sequence is one such phosphatase. Phosphatases are
CC enzymes that catalyse the dephosphorylation of proteins modified by
CC phosphorylation of serine, threonine or tyrosine residues. The
CC phosphatases are useful for treating a variety of diseases: for example
CC cancer e.g. breast, urogenital, prostate, head, neck, lung cancers,
CC synovial sarcomas, renal cell carcinoma, non-small cell lung cancer,
CC hepatocellular carcinoma, pancreatic endocrine tumours, stomach cancer,
CC glioblastoma, colorectal cancer and thyroid cancer, pathophysiological
CC hypoxia, cardiac dysfunction and/or vascular disorders, myopathies,
CC congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease,
CC ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan
CC Zonana syndrome, schizophrenia and hamartomas.
XX
SQ Sequence 184 AA;
XX
Query Match 92.7%; Score 831.5; DB 22; Length 184;
Best Local Similarity 88.6%; Pred. No. 9e-94;
Matches 163; Conservative 0; Mismatches 4; Indels 17; Gaps 2;
```

```
RESULT 4
AAB67167
ID AAB67167 standard; Protein; 184 AA.
XX
AC AAB67167;
XX
DT 12-APR-2001 (first entry)
XX
DE Human dual-specificity phosphatase DSP-3.
XX
KW Human; DSP-3; dual-specificity phosphatase; cell proliferation;
KW cell signalling; cancer; graft-versus-host disease; autoimmune disease;
KW allergy; metabolic disease; Duchenne muscular dystrophy.
XX
OS Homo sapiens.
XX
PN WO200102581-A1.
XX
PD 11-JAN-2001.
XX
PE 20-APR-2000; 2000WO-US10868.
XX
PR 02-JUL-1999; 99US-0142338.
XX
PR 07-APR-2000; 2000WO-US09185.
XX
PA (CEPT-) CEPTYR-INC.
XX
PI LUCHE RM, WEI B;
XX
DR WPI; 2001-138148/14.
XX
DR N-PSDB; AAF32191.
XX
XX
PT New dual-specificity phosphatase-3 polypeptide and its variants useful
PT for treating disorders associated with DSP-3 activity, defects in cell
PT proliferation, differentiation or survival, e.g. Duchenne muscular
PT dystrophy, cancer
XX
PS Claim 1; Fig 2; 70pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human dual-specificity phosphatase DSP-3. The DSP-3 protein is involved
CC in cell signalling and the sequences can be used in the treatment of
CC cancer, metabolic and autoimmune diseases, allergies, graft-versus-host
CC disease, abnormal cell proliferation and Duchenne muscular dystrophy.
XX
SQ Sequence 184 AA;
XX
Query Match 92.7%; Score 831.5; DB 22; Length 184;
Best Local Similarity 88.6%; Pred. No. 9e-94;
Matches 163; Conservative 0; Mismatches 4; Indels 17; Gaps 2;
```

```
RESULT 5
AAB66431
ID AAB66431 standard; Protein; 184 AA.
XX
AC AAB66431;
XX
DT 06-APR-2001 (first entry)
XX
DE Human DSP-3 protein.
XX
KW Human; DSP-3; cytosolic; immunosuppressive; anti-allergic;
XX dual specificity phosphatase-3; cell proliferation; metabolic diseases;
KW Duchenne muscular dystrophy; cancer; graft-versus-host disease;
KW autoimmune disease; allergy.
XX
OS Homo sapiens.
XX
PN WO200102582-A1.
XX
PD 11-JAN-2001.
XX
PE 29-JUN-2000; 2000WO-US18207.
XX
PR 02-JUL-1999; 99US-0142338.
XX 07-APR-2000; 2000WO-US09185.
XX 20-APR-2000; 2000WO-US10868.
XX
PA (CEPT-) CEPTYR INC.
XX
PI Lucite RM, Wei B;
XX
DR WPI; 2001-138149/14.
XX N-PSDB; AAF29601.
XX
PT New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form
PT polypeptides, useful for identifying modulators DSP-3 or DSP-3
PT alternate form activity, especially for treating e.g. cancer,
PT autoimmune diseases or allergies -
XX
PS Claim 1; Fig 2; 86pp; English.
XX
CC The present sequence is given in a specification providing human dual
CC specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide.
CC The polypeptides are useful for dephosphorylating a substrate of DSP-3.
CC e.g. MAP-kinase. They may be used to treat or prevent diseases associated
CC with cell proliferation, immunosuppression, metabolic diseases, or
CC abnormal cell growth or cell cycle abnormalities. They are also useful
CC for identifying agents that modulate their activity. The modulators are
CC useful for treating disorders associated with DSP-3 or DSP-3 variant
CC activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host
CC disease, autoimmune diseases, allergies, metabolic diseases, abnormal
CC cell growth, abnormal cell proliferation and cell cycle abnormalities.
CC The modulating agents are useful for modulating, modifying or altering
CC cellular responses, e.g. in vivo or in vitro cell proliferation,
CC differentiation or survival.
XX
SQ Sequence 184 AA;

Query Match 92.7%; Score 831.5; DB 22; Length 184;
Best Local Similarity 88.6%; Pred. No. 9e-94;
Matches 163; Conservative 0; Mismatches 4; Indels 17; Gaps 2;

OY 1 MGNGNKILPLGLYIGNFKDARDAEQLSKNKVTHILSVHDSFG-----LCW----- 45
DB 1 mgnnmkllppllygnfkardaeqlsknkvtllsvndsrpmlegvkylcldpadps 60
OY 46 --RRHRESIKFTHECHLRGESCIVHCLAGVSRVTLVIAYIMVTPFGMEDALHTVRA 103
DB 61 qnltrhfesikflheclrgescivhclagvsrvtlviayimvtpfgmedalhtvra 120
OY 104 GRSCANPVWGFQROLQEEKEHVIHQYRQWLKEEYGESPLQDAEAKNLIAPGILKFWAF 163
|||||
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DB 121 grscanpvwfgfqrqlqefekhevhqyrqwlkeeygesplqdaeeaknliapgilkfmaf 180
OY 164 LRRL 167
DB 181 lrri 184

RESULT 6
AAB73213
ID AAB73213 standard; Protein; 184 AA.
XX
AC AAB73213;
XX
DT 11-MAY-2001 (first entry)
XX
DE Murine phosphatase AA103595_m.
XX
KW Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia;
KW cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia;
KW congenital muscle disorder; Papillon-LeFevre syndrome; Cowden disease;
KW Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;
KW schizophrenia; hamartoma.
XX
OS Mus sp.
XX
PN WO200112819-A2.
XX
PD 22-FEB-2001.
XX
PE 11-AUG-2000; 2000WO-US22158.
XX
PR 13-AUG-1999; 99US-0149005.
XX
PA (SUGEN-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;
XX
DR WPI; 20014211226/21.
XX N-PSDB; AAF63565.
XX
PT New protein phosphatase polypeptide for diagnosing and treating
PT phosphatase related disorders such as cancer, schizophrenia, cardiac
PT dysfunction and/or vascular disorders -
XX
PS Claim 6; Fig 5; 138pp; English.
XX
CC The present invention relates to phosphatase proteins and coding
CC sequences. The present sequence is one such phosphatase. Phosphatases are
CC enzymes that catalyse the dephosphorylation of proteins modified by
CC phosphorylation of serine, threonine or tyrosine residues. The
CC phosphatases are useful for treating a variety of diseases: for example
CC cancer e.g. breast, urogenital, prostate, head, neck, lung cancers,
CC synovial sarcomas, renal cell carcinoma, non-small cell lung cancer,
CC hepatocellular carcinoma, pancreatic endocrine tumours, stomach cancer,
CC glioblastoma, colorectal cancer and thyroid cancer, pathophysiological
CC hypoxia, cardiac dysfunction and/or vascular disorders, myopathies,
CC congenital muscle disorders, Papillon-LeFevre syndrome, Cowden disease,
CC ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan
CC Zonana syndrome, schizophrenia and hamartomas.
XX
SQ Sequence 184 AA;

Query Match 88.2%; Score 791.5; DB 22; Length 184;
Best Local Similarity 82.6%; Pred. No. 7.3e-89;
Matches 152; Conservative 11; Mismatches 4; Indels 17; Gaps 2;

OY 1 MGNGNKILPLGLYIGNFKDARDAEQLSKNKVTHILSVHDSFG-----LCW----- 45
DB 1 msgmsqllppllygnfkardaeqlsrnkvtllsvndsrpmlegvkylcldpadtps 60
OY 46 --RRHRESIKFTHECHLRGESCIVHCLAGVSRVTLVIAYIMVTPFGMEDALHTVRA 103
|||||
```


for identifying agents that modulate their activity. The modulators are useful for treating disorders associated with DSP-3 or DSP-3 variant activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host disease, autoimmune diseases, allergies, metabolic diseases, abnormal cell growth, abnormal cell proliferation and cell cycle abnormalities. The modulating agents are useful for modulating, modifying or altering cellular responses, e.g. in vivo or in vitro cell proliferation, differentiation or survival.

Sequence 205 AA:

Query Match 79.8%; Score 715.5; DB 22; Length 205;
Best Local Similarity 81.7%; Pred. No. 1.8e-79;
Matches 138; Conservative 10; Mismatches 4; Indels 17; Gaps 2;

QY 1 MGNGMKNKILPGLYIGNFKARDAEOLSKNKVTHILSVHDSFG-----LCW----- 45
DB 1 msgsmgqllpglylgnfkardaeqlsrnkvtllsvhdtarpmlegvlylcipaadtps 60
QY 46 --RTRHFKESIKFIHECRIRGESCLVHCLAGYSRSVTLVIAYIMVTDFGWDALHTVRA 103
DB 61 gnltrhfkesikfihecrirgesclvnhclagysrsvtlviayimvtldfgwedahlvtvra 120

QY 104 GRSCANPNVGFQROLOEFKEHEVHOYROWLKEEYGESPLQDAEAKNLL 152
DB 121 grscanpnlgfgrqfqefekhevhgryqlreeygenplrddeeknll 169

RESULT 9
AAB81106
AAB81106 standard; Protein; 205 AA.

29-JUN-2001 (first entry)

Murine JNK activating phosphatase (JNAP).

C-Jun amino-terminal kinase; JNK; JNK activating phosphatase; JNAP;
dual-specificity phosphatase; ischemic heart disease; kidney failure;
cardiac hypertrophy; burn; liver damage; respiratory distress syndrome;
septic shock; rheumatoid arthritis; autoimmune disorder; mouse;
inflammatory disease; chromosome 13.

Mus sp.

WO200121812-A1.

29-MAR-2001.

21-SEP-2000; 2000WO-US25948.

21-SEP-1999; 99US-0155068.

20-SEP-2000; 2000US-0665819.

(AMGE-) AMGEN INC.

(BAYU) BAYLOR COLLEGE MEDICINE.

Tan T, Zhou G, Belmont JW, Fletcher FA, Chen AJ, Jurecic R;

WPI; 2001-316103/33.

N-PSDB; AAF86153.

New human or mouse C-Jun amino-terminal kinase (JNK) activating phosphatase is useful for diagnosing or treating diseases associated with JNK activating phosphatase or JNK-mediated disorders, e.g. inflammatory diseases

Claim 8; Fig 2; 116pp; English.

This invention relates to human or murine C-Jun amino-terminal kinase (JNAP) activating phosphatase (JNAP). The present sequence represents

murine JNAP. The JNAP gene has been mapped to murine chromosome 13. The JNAP protein has an amino-terminal dual-specificity phosphatase domain and lacks a non-catalytic carboxy-terminal domain. The protein has functional activities comprising dual-specificity phosphatase activity and JNK pathway upregulation activity. The JNAP polypeptide can be used for diagnosing a JNK-mediated disorder or a susceptibility to a JNK-mediated disorder, and for identifying a compound which binds to it. The JNAP polypeptide and nucleic acid molecules are useful in screening for therapeutic agents to treat, prevent and/or detect conditions relating to JNK-mediated disorders, e.g. ischemic heart disease, cardiac hypertrophy, burns due to heat or radiation, kidney failure, liver damage due to oxidative stress or alcohol, respiratory distress syndrome, septic shock, rheumatoid arthritis, autoimmune disorders, or other types of inflammatory diseases. The polypeptides may also be used for screening therapeutic agents for treating a disease involving cytokine production in an animal, and for identifying agents that modulate the JNK signal transduction pathways. The nucleic acid molecules encoding JNAP are useful for mapping the locations of the JNK activating phosphatase gene and related genes on chromosomes; as anti-sense inhibitors of JNK activating phosphatase polypeptide expression; or for gene therapy.

Sequence 205 AA:

Query Match 78.3%; Score 702.5; DB 22; Length 205;
Best Local Similarity 80.5%; Pred. No. 7.1e-78;
Matches 136; Conservative 10; Mismatches 6; Indels 17; Gaps 2;

QY 1 MGNGMKNKILPGLYIGNFKARDAEOLSKNKVTHILSVHDSFG-----LCW----- 45
DB 1 msgsmgqllpglylgnfkardaeqlsrnkvtllsvhdtarpmlegvlylcipaadtps 60
QY 46 --RTRHFKESIKFIHECRIRGESCLVHCLAGYSRSVTLVIAYIMVTDFGWDALHTVRA 103
DB 61 gnltrhfkesikfihecrirgesclvnhclagysrsvtlviayimvtldfgwedahlvtvra 120

QY 104 GRSCANPNVGFQROLOEFKEHEVHOYROWLKEEYGESPLQDAEAKNLL 152
DB 121 grscanpnlgfgrqfqefekhevhgryqlreeygenplrddeeknll 169

RESULT 10
AAB66442
AAB66442 standard; Protein; 145 AA.

AAB66442;

06-APR-2001 (first entry)

Human MAP-kinase phosphatase DSP-3.

Human; MAP-kinase; mitogen-activated protein kinase; DSP-3; cytosolic;
immunosuppressive; anti-allergic; dual specificity phosphatase-3;
cell proliferation; metabolic diseases; Duchenne muscular dystrophy;
cancer; graft-versus-host disease; autoimmune disease; allergy; DSP-3.

Homo sapiens.

WO200102582-A1.

11-JAN-2001.

29-JUN-2000; 2000WO-US18207.

02-JUL-1999; 99US-0142338.

07-APR-2000; 2000WO-US09185.

20-APR-2000; 2000WO-US10868.

(CEPT-) CEPTV INC.

Lucho RM, Wei B;

WPI; 2001-138149/14.

XX New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form
PT polypeptides, useful for identifying modulators DSP-3 or DSP-3
PT alternate form activity, especially for treating e.g. cancer,
PT autoimmune diseases or allergies
XX
XX Example 1; Fig 3; 86pp; English.
XX
CC The present sequence is given in a specification providing human dual
CC specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide.
CC The polypeptides are useful for dephosphorylating a substrate of DSP-3,
CC e.g. MAP-kinase. They may be used to treat or prevent diseases associated
CC with cell proliferation, immunosuppression, metabolic diseases, or
CC abnormal cell growth or cell cycle abnormalities. They are also useful
CC for identifying agents that modulate their activity. The modulators are
CC useful for treating disorders associated with DSP-3 or DSP-3 variant
CC activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host
CC disease, autoimmune diseases, allergies, metabolic diseases, abnormal
CC cell growth, abnormal cell proliferation and cell cycle abnormalities.
CC The modulating agents are useful for modulating, modifying or altering
CC cellular responses, e.g. in vivo or in vitro cell proliferation,
CC differentiation or survival.
CC
XX
XX Sequence 145 AA:
SO
Query Match 71.8%; Score 644; DB 22; Length 145;
Best Local Similarity 87.6%; Pred. No. 6.6e-71;
Matches 127; Conservative 0; Mismatches 4; Indels 14; Gaps 2;
OY 1 MGNGMKNKILPGIYIGNFKDARDADQLSKNKVTHILSVHDSFG-----ICW-----R 46
Db 1 mgngmknkllpilygnfkdardaeqlsknkvtllsvhdsarpmlegvkylicipadps 60
OY 47 TRHFKESIKFIEHCRRLRGESCLVHCLAGVSRSVTLYIATMYTDFGEMDALHTVRAGRS 106
Db 61 trhkessikfihcecrilrgescvchclagsrsvtlyiatmytdfgwedahlvtrags 120
OY 107 CANPNVGFQROLOEFKEHEVHQYRQ 131
Db 121 canpnvgfqrqlqefekhevhyqyr 145
RESULT 11
AAE04840
ID AAE04840 standard; Protein: 329 AA.
XX
AC AAE04840;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human SGP008 phosphatase polypeptide.
XX
KW Human; SGP008 phosphatase polypeptide; phosphatase-related disease;
KW immune-related disorder; ocular disease; organ transplant rejection;
KW infection; diabetes; pain; sexual dysfunction; Alzheimer's disease;
KW metabolic disorder; haematopoietic cancer; mood disorder; cardiac;
KW Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis;
KW cardiovascular disease; brain; neuronal-associated disease; dyskinesia;
KW attention disorder; cognitive disorder; psychotic disorder; cystostatic;
KW neurological disorder; vincristine; nocitropic; cerebroprotective; therapy;
KW neuroprotective; antibacterial; vulnary; tranquilliser; antisthmatic;
KW hypotensive; immunosuppressive; antipsoriatic; analgesic; hypertensive;
KW antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase;
KW MKP; mitogen; chromosome 20q11.2.
XX
OS Homo sapiens.
XX
FH Key
FH 1..173 Location/Qualifiers
FT Domain
FT /label= Catalytic_domain
FT 98..235
FT Domain
FT /label= Phosphatase_domain

FT Misc-difference 323..329
FT /note= "Encoded by CTCGC"
XX
XX W0200146394-A2.
XX
XX 28-JUN-2001.
XX
XX 21-DEC-2000; 2000WO-US34736.
XX
XX 21-DEC-1999; 99US-0173255.
XX 28-DEC-1999; 99US-0175766.
XX 25-JAN-2000; 2000US-0178078.
XX 31-JAN-2000; 2000US-0179301.
XX (SUGC-) SUGEN INC.
XX
XX Plowman GD, Martinez R, Whyte D, Manning G, Sudarsanam S, Hill RJ;
XX Flanagan P;
XX WPI: 2001-418058/44.
XX N-PSDB; AAD09498.
XX
XX Novel phosphatase polypeptide useful for treating cancers,
XX immune-related diseases and disorders, cardiovascular disease, brain or
XX neuronal associated diseases and metabolic disorders
XX
XX Claim 7; Fig 2; 186pp; English.
XX
XX The present invention relates to phosphatase polypeptides, nucleotide
XX sequences encoding them, as well as various products and methods useful
XX for the diagnosis and treatment of various phosphatase-related diseases
XX and conditions. Substance that modulates the activity of phosphatase
XX polypeptide is used to treat immune-related diseases and disorders,
XX cardiovascular disease, brain or neuronal-associated diseases and
XX metabolic disorders, including cancers of tissues, cancers of
XX haematopoietic origin, diseases of central and peripheral nervous
XX system, Alzheimer's disease, Parkinson's disease, multiple sclerosis,
XX amyotrophic lateral sclerosis, viral infections, infections caused by
XX prions, bacteria and fungi, ocular diseases, diabetes, migraines, pain,
XX sexual dysfunction, mood disorders, attention disorders, cognition
XX disorders, hypotension, hypertension, psychotic disorders, neurological
XX disorders, dyskinesias and organ transplant rejection. The present
XX amino acid sequence is human SGP008 phosphatase polypeptide. This
XX sequence is classified as dual specificity phosphatase (DSP) and MAP
XX kinase phosphatase (MKP). SGP008 gene maps to chromosomal position
XX 20q11.2.
XX
XX Sequence 329 AA:
SO
Query Match 51.1%; Score 458.5; DB 22; Length 329;
Best Local Similarity 50.3%; Pred. No. 1.2e-47;
Matches 85; Conservative 27; Mismatches 40; Indels 17; Gaps 1;
OY 1 MGNGMKNKILPGIYIGNFKDARDADQLSKNKVTHILSVHDSFGICWR----- 46
Db 95 mgngmktkvlpyglygnfkdardakldqgrnkthihsheppllqdlitrlpvadtpe 154
OY 47 ---TRHFKESIKFIEHCRRLRGESCLVHCLAGVSRSVTLYIATMYTDFGEMDALHTVR 103
Db 155 vlhkfhkechffihccrclngncclvhcfcagrsstltvaymtvtgfwrdvleaika 214
OY 104 GSCANPNVGFQROLOEFKEHEVHQYRQMLKEEYSGSPIDDAEAKNLL 152
Db 215 trlpianpvgfqrqlqefekhevhyqyrqlqleefgwasgkrltrqleefgspirdeetrall 263
RESULT 12
AAB41570
ID AAB41570 standard; Protein: 96 AA.
XX
AC AAB41570;
XX

DT 08-FEB-2001 (first entry)
 XX Human ORFX ORF1334 polypeptide sequence SEQ ID NO:2668.
 DE
 XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnerability; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; antiparkinsonian; neurotropic; neuroprotective;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antineoplastic;
 KW antiviral; antibacterial; antifungal; antineoplastic; antihypertensive;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200058473-A2.
 PN
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 XX
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 XX Shinketsu RA, Leach M;
 PI
 DR WPI: 2000-602362/57.
 DR N-PSDB: AAC75779.
 XX
 XX Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 XX Claim 11; Page 1911; 5507pp: English.
 PS
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerability;
 CC antiparkinsonian; antiparkinsonian; neurotropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiparkinsonian; immunosuppressive;
 CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antineoplastic; antibacterial; antiviral; antifungal; antineoplastic;
 CC antihypertensive; antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 CC
 XX Sequence 96 AA;
 SQ
 Query Match 48.3%; Score 433.5; DB 21; Length 96;
 Best Local Similarity 89.6%; Pred. NO. 2.5e-45;
 Matches 86; Conservative 1; Mismatches 6; Indels 3; Gaps 2;

OY 1 MGNGANKILPGLYTGNFKARDAEQLSKNKVTHILSVHDS--PGLCWRTRRHREKSTKFTIH 58
 DB 2 mgngmknkllpglytgnfkardaeqlsknk-ngpfsvcpvrwpglcrtrhfesikfih 60
 OY 59 ECLRGESCLVHCLACVSRSVTLVIAYIMTWDFEGM 94
 DB 61 eclrlgesclvncldagsvsvtlviayimtwdfegw 96
 RESULT 13
 AAB29641
 ID AAB29641 standard; Protein: 482 AA.
 AC
 XX AAB29641;
 XX
 DT 23-FEB-2001 (first entry)
 XX
 DE Human dual-specificity MAP kinase phosphatase DSP-10.
 XX
 XX Human DSP-10; dual-specificity phosphatase; antibody;
 KW dual-specificity MAP kinase phosphatase; drug screening;
 KW protein tyrosine phosphatase family; PTP; recombinant production;
 KW proliferative response; cell differentiation; cell survival;
 KW proliferative disorder; cell cycle abnormality; metabolic disease;
 KW Duchenne muscular dystrophy; cancer; graft-versus-host disease;
 KW autoimmune disease; allergy.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200065068-A1.
 PN
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-US10966.
 XX
 PR 23-APR-1999; 99US-0130806.
 PR
 XX
 XX (CEPT-) CEPTYR INC.
 PA
 XX
 XX Luche RM, Wei B;
 PI
 DR WPI: 2000-687352/67.
 DR N-PSDB: AAC64262.
 XX
 XX Novel dual specificity phosphatase-10 which dephosphorylates activated
 PT mitogen-activated protein kinase, for identifying agents inhibiting
 PT DSP-10 activity and modulate cell proliferation, differentiation,
 PT survival -
 XX
 XX Claim 1; Fig 2; 65pp: English.
 PS
 XX The invention relates to a human dual-specificity mitogen-activated
 CC protein (MAP) kinase phosphatase, DSP-10, and to nucleic acids encoding
 CC it. The invention also relates to variants of DSP-10 which retain
 CC activity, expression vectors and host cells comprising DSP-10 encoding
 CC DNA, the recombinant production of DSP-10, an anti-DSP-10 antibody, and
 CC a DSP-10 substrate-trapping mutant protein that has a reduced ability to
 CC dephosphorylate a substrate relative to the wild-type DSP-10. The
 CC invention additionally encompasses use of a DSP-10 modulator to modulate
 CC a proliferative response, cell differentiation or cell survival. The
 CC DSP-10 protein is useful for screening an agent that binds to DSP-10
 CC and/or modulates DSP-10 activity, and is also useful for raising
 CC antibodies. DNA encoding DSP-10 or a reporter protein is also useful for
 CC screening an agent that modulates DSP-10 activity. The identified agents
 CC that modulate DSP-10 activity are useful for treating Duchenne muscular
 CC dystrophy, cancer, graft-versus-host disease, autoimmune diseases,
 CC allergies, metabolic diseases, abnormal cell growth, abnormal cell
 CC proliferation and cell cycle abnormalities. The DSP-10 modulating
 CC agents inhibit or enhance signal transduction via a MAP-kinase
 CC cascade, leading to cell proliferation. An agent that modulates DSP-10
 CC activity may alter expression and/or stability of DSP-10, DSP-10
 CC protein activity and/or the ability of DSP-10 to dephosphorylate a

CC substrate. Compounds so identified as capable of influencing DSP-10
 CC function (e.g., phosphorylation and/or phosphoserine/threonine
 CC dephosphorylation) are valuable for therapeutic and/or diagnostic
 CC purposes, since they permit treatment and/or detection of disease
 CC associated with DSP-10 activity. Such compounds are also valuable in
 CC research directed to molecular signaling mechanisms that involve
 CC DSP-10 and in the discovery and development of future DSP-10 compounds
 CC exhibiting greater specificity. The DSP-10 polypeptides are useful for
 CC dephosphorylating a DSP-10 substrate. DSP-10-specific antibodies
 CC and DSP-10 antisense probes are useful for detecting DSP-10 expression in
 CC a sample, and may thus be used in the detection of a proliferative
 CC disorder. The present sequence represents human DSP-10.

SO Sequence 482 AA;

Query Match 23.4%; Score 210; DB 21; Length 482;
 Best Local Similarity 36.0%; Pred. No. 6.8e-17;
 Matches 50; Conservative 21; Mismatches 48; Indels 20; Gaps 2;

QY 5 MNKILPGIYIGFKDARAEOLSK-----NKVTHILSVDSFGLCKRTR----- 48
 Db 322 ltlplpflflgndqagldtmqrlnlyvlnvthlplhyekylfnykrlpatdsnkq 381
 QY 49 -----HFKSIRKFIHECRIRGESCIVHCLAGVSRTIVATIMVYTDGMDALHTVAG 104
 Db 382 nlrgyfeeaftleahbqcgkylilhcgayvsatlylaimkhtmtmdaykfkvqk 441
 QY 105 RSCANPNVGFORLOEFK 123
 Db 442 rplspnlmfmgqllefee 460

RESULT 14
 AAB18655
 ID AAB18655 standard; Protein: 482 AA.

XX AAB18655;
 DT 22-JAN-2001 (first entry)

XX A human regulator of intracellular phosphorylation.

XX Human; intracellular phosphorylation regulator; HRIP; stroke; myeloma;
 KW neurological disorder; Parkinson's disease; demyelinating disease;
 KW meningitis; developmental disorder; neuromuscular disorder; cancer;
 KW myasthenia gravis; cell proliferative disorder; actinic keratosis;
 KW arteriosclerosis; atherosclerosis; leukemia; melanoma; bronchitis;
 KW autoimmune disorder; inflammatory disorder; Addison's disease;
 KW acquired immunodeficiency disease; allergy; diabetes mellitus;
 KW rheumatoid arthritis; microbial infection; trauma.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "potential phosphorylation site"
 FT Modified-site 52 /note= "potential phosphorylation site"
 FT Modified-site 57 /note= "potential phosphorylation site"
 FT Modified-site 67 /note= "potential glycosylation site"
 FT Modified-site 140 /note= "potential phosphorylation site"
 FT Modified-site 146 /note= "potential phosphorylation site"
 FT Modified-site 160 /note= "potential phosphorylation site"
 FT Modified-site 184 /note= "potential phosphorylation site"
 FT Modified-site 201 /note= "potential glycosylation site"
 FT Modified-site /note= "potential phosphorylation site"

FT Modified-site 211 /note= "potential phosphorylation site"
 FT Modified-site 217 /note= "potential phosphorylation site"
 FT Modified-site 217 /note= "potential phosphorylation site"
 FT Modified-site 224 /note= "potential phosphorylation site"
 FT Modified-site 258 /note= "potential phosphorylation site"
 FT Modified-site 275 /note= "potential phosphorylation site"
 FT Modified-site 313 /note= "potential phosphorylation site"
 FT Modified-site 321.461 /note= "potential phosphorylation site"
 FT Active-site 353 /note= "dual-specificity phosphatase catalytic site"
 FT Modified-site 378 /note= "potential glycosylation site"
 FT Modified-site 430 /note= "potential phosphorylation site"
 FT Modified-site 467 /note= "potential phosphorylation site"
 FT Modified-site 472 /note= "potential phosphorylation site"
 FT Modified-site /note= "potential phosphorylation site"

PN W0200055332-A2.

PD 21-SEP-2000.

PF 17-MAR-2000; 2000WO-US07277.

PR 18-MAR-1999; 99US-0125593.

PR 20-MAY-1999; 99US-0135049.

PR 09-JUL-1999; 99US-0143188.

XX (INCY-) INCYTE PHARM INC.

XX Bandman O, Tang YT, Yue H, Hillman JL, Baughn MR, Azimzai Y;
 PI Lu DM, Au-Young J;

XX WPI: 2000-602121/57.

DR N-PSDB: AAA75672.

XX Novel human intracellular phosphorylation regulator polypeptides and
 PT polynucleotides for diagnosis, prevention and treatment of
 PT neurological, cell proliferative and autoimmune/inflammatory disorders

PS Claim 1; Page 73-74; 96pp; English.

XX The present sequence represents a human regulator of intracellular
 CC phosphorylation (HRIP). HRIP is useful for screening agonists and
 CC antagonists of HRIP polypeptide. HRIP and its agonist or antagonist
 CC are useful for treating a disease or condition associated with
 CC decreased or increased expression of functional HRIP. Diseases treated
 CC or diagnosed include neurological disorders such as stroke, Parkinson's
 CC disease, demyelinating diseases, bacterial and viral meningitis and
 CC other developmental disorders of the central nervous system,
 CC neuromuscular disorders, myasthenia gravis, cell proliferative disorders
 CC such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer
 CC including leukemia, melanoma, myeloma and cancer of the adrenal gland,
 CC bladder, bone, bone marrow, liver, lung, muscle, ovary, autoimmune/
 CC inflammatory disorder such as Addison's disease, acquired
 CC immunodeficiency diseases, allergies, bronchitis, diabetes mellitus,
 CC rheumatoid arthritis, microbial infection and trauma.

SO Sequence 482 AA;

Query Match 23.4%; Score 210; DB 21; Length 482;
 Best Local Similarity 36.0%; Pred. No. 6.8e-17;

```

Matches 50; Conservative 21; Mismatches 48; Indels 20; Gaps 2;
QY 5 MNKILPGLYIGNFKDARDAEOLSK-----NKVTHILSVHDSPGICWRT----- 48
Db 322 lrpilpflfigneqdvrdidtmqrlngyvinvtthlpkyekglfnykrilpatsnkg 381
QY 49 ----HKESIKFTHECRLEGESCLVHCLAGVSRSVTLVIAYIMVTYDFGEMDALHTVRAG 104
Db 382 nlrqyfeeaefeieeahqcgkylhhcgaqvsarsativaiymkhlrmumtdaykfvkkg 441
QY 105 RSCANPNVGFQROLOEFK 123
Db 442 rpiispnlmfmqlllefee 460

```

RESULT 15

AAB73225
ID AAB73225 standard; Protein; 482 AA.

AC AAB73225;

DT 11-MAY-2001 (first entry)

DE Human phosphatase MKP-5_h.

KW Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia;

KW cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia;

KW congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease;

KW Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;

KW schizophrenia; hamartoma.

OS Homo sapiens.

PN WO200112819-A2.

PD 22-FEB-2001.

PF 11-AUG-2000; 2000WO-US22158.

PR 13-AUG-1999; 99US-0149005.

PA (SUGC-) SUGEN INC.

PI Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;

DR WPI: 2001-211226/21.

DR N-PSDB: AAF63577.

XX New protein phosphatase polypeptide for diagnosing and treating

XX phosphatase related disorders such as cancer, schizophrenia, cardiac

XX dysfunction and/or vascular disorders -

XX Claim 6; Fig 5; 138pp; English.

XX The present invention relates to phosphatase proteins and coding

XX sequences. The present sequence is one such phosphatase. Phosphatases are

XX enzymes that catalyse the dephosphorylation of proteins modified by

XX phosphorylation of serine, threonine or tyrosine residues. The

XX phosphatases are useful for treating a variety of diseases: for example

XX cancer e.g. breast, urogenital, prostate, head, neck, lung cancers,

XX synovial sarcoma, renal cell carcinoma, non-small cell lung cancer,

XX hepatocellular carcinoma, pancreatic endocrine tumours, stomach cancer,

XX glioblastoma, colorectal cancer and thyroid cancer, pathophysiological

XX hypoxia, cardiac dysfunction and/or vascular disorders, myopathies,

XX congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease,

XX ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan

XX Zonana syndrome, schizophrenia and hamartomas.

XX Sequence 482 AA;

```

Matches 50; Conservative 20; Mismatches 49; Indels 20; Gaps 2;
QY 5 MNKILPGLYIGNFKDARDAEOLSK-----NKVTHILSVHDSPGICWRT----- 48
Db 322 lrpilpflfigneqdvrdidtmqrlngyvinvtthlpkyekglfnykrilpatsnkg 381
QY 49 ----HKESIKFTHECRLEGESCLVHCLAGVSRSVTLVIAYIMVTYDFGEMDALHTVRAG 104
Db 382 nlrqyfeeaefeieeahqcgkylhhcgaqvsarsativaiymkhlrmumtdaykfvkkg 441
QY 105 RSCANPNVGFQROLOEFK 123
Db 442 rpiispnlmfmqlllefee 460

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Search completed: February 12, 2002, 16:12:52
Job time: 191 sec

Query Match 23.4%; Score 210; DB 22; Length 482;
Best Local Similarity 36.0%; Pred. No. 6.8e-17;

A: Experimental source: strain 972h-; cosmid c17A3
 C: Genetics:
 A: Gene: p1041
 A: Map position: 2

Query Match 22.5%; Score 202; DB 2; Length 330;
 Best Local Similarity 32.3%; Pred. No. 1.2e-12;
 Matches 52; Conservative 26; Mismatches 59; Indels 24; Gaps 4;

OY 3 NGNNKILPGLYIGNFKDARDAEQLSKNKYTHILSVHDS-SPGL------CWR----- 46
 DB 45 NDLSEIKMLYISMTASELVSIDKGDIDYLSAMSINPLNSVPEQOHLMLQIEDSSQ 104
 OY 47 --TRHFKESIKFTHECRLESGESCTVHCLAGVSRSVTLVIATYMTVDFGMDALHTVRAG 104
 DB 105 NILQYREKSKFTAFALSKNAKLVHCPAGISRSVTLVAAYLTKENNMNTEALSHINER 164
 OY 105 RSCANPNVGFQROLOFEK-----HEVHQYRQWLKEEXGE 139
 DB 165 RSGISPNANFLRQLRVYFECNYQLDRSLRPYRQWLFRRYGD 205

RESULT 3
 T32494
 Hypothetical protein C05B10.1 - *Caenorhabditis elegans*
 C: Species: *Caenorhabditis elegans*
 C: Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C: Accession: T32494

R: Geisel, C.; Wamsley, P.
 Submitted to the EMBL Data Library, December 1997
 A: Description: The sequence of C. elegans cosmid C05B10.
 A: Reference number: 221178
 A: Accession: T32494
 A: Status: preliminary; translated from GB/EMBL/DBDJB
 A: Molecule type: DNA
 A: Residues: 1-365 <GET>
 A: Cross-references: EMBL:AF036665; PIDN: AAB88308.1; GSPDB: G000022; CESP: C05B10.1
 A: Experimental source: strain Bristol N2; clone C05B10
 C: Genetics:
 A: Gene: CESP: C05B10.1
 A: Map position: 4
 A: Introns: 22/2; 46/2; 74/3; 163/2; 204/2; 248/1; 287/2

Query Match 21.6%; Score 194; DB 2; Length 365;
 Best Local Similarity 31.4%; Pred. No. 8.4e-12;
 Matches 43; Conservative 27; Mismatches 47; Indels 20; Gaps 2;

OY 7 KILPGLYIGNFKDARDAEQLSKNKYTHILSV-----HDSPLGLCW-----R 46
 DB 183 KLTNELYIGNAETAKNRDVLTKYSISHVINVTSLPNTFEEDPNRRYLRLISADNASHNL 242
 OY 47 TRHFKESIKFTHECRLESGESCTVHCLAGVSRSVTLVIATYMTVDFGMDALHTVRAGS 106
 DB 243 TKFEFSAISFIDARRNDASACVHCLAGISRSVTLCLAYLTKENCTLDSAEVWQKRNA 302
 OY 107 CANPNVGFQROLOFEK 123
 DB 303 STAPNFHEMGQLTDYER 319

RESULT 4
 I38890
 dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 5 - human
 N: Alternate names: dual specificity phosphatase B23; dual-specificity phosphatase hVH-3;
 C: Species: Homo sapiens (man)
 C: Date: 16-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 11-Jun-1999
 C: Accession: I38890; A55313
 R: Kwak, S.P.; Dixon, J.E.
 J. Biol. Chem. 270, 1156-1160, 1995
 A: Title: Multiple dual specificity protein tyrosine phosphatases are expressed and regulated
 A: Reference number: A55432; MUID: 95138103

A: Accession: I38890

A: Molecule type: mRNA

A: Residues: 1-384 <RES>

A: Cross-references: EMBL: U16996; NID: g642012; PIDN: AAB06261.1; PID: g642013

A: Experimental source: placenta

R: Ishibashi, T.; Bottaro, D.P.; Michieli, P.; Kelley, C.A.; Aaronson, S.A.
 J. Biol. Chem. 269, 29897-29902, 1994

A: Title: A novel dual specificity phosphatase induced by serum stimulation and heat

A: Reference number: A55313; MUID: 95050849

A: Accession: A55313

A: Molecule type: mRNA

A: Residues: 1-8, 'GHV', 12-70, 'R', 72-104, 'F', 107-362, 'RCLPTQSSSAPALMORPAPAKTGEESAPQ'

A: Cross-references: GB: U15932; NID: g606971; PIDN: AAA64693.1; PID: g606972

A: Experimental source: mammary epithelial cells

C: Genetics:

A: Gene: GDB: DUSP5

A: Cross-references: GDB: 385447

A: Map position: 10q25-10q25

C: Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specific

C: Keywords: phosphoprotein; phosphoric monoester hydrolase

F: 186-317/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL

F: 263/Active site: Cys (phosphocysteine intermediate) #status predicted

F: 263/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.7%; Score 186; DB 1; Length 384;
 Best Local Similarity 33.6%; Pred. No. 5.7e-11;
 Matches 46; Conservative 21; Mismatches 55; Indels 18; Gaps 1;

OY 4 GNNKILPGLYIGNFKDARDAEQLSKNKYTHILSVHDSPLGLCWRT----- 48
 DB 178 GVEILLPFLYIGSAVHASKCEFLANLHITALLNVSRRTSACMTHLHYKWIPEDSHTAD 237
 OY 49 ---HFKESIKFTHECRLESGESCTVHCLAGVSRSVTLVIATYMTVDFGMDALHTVRAGR 105
 DB 238 ISSHFQEAIDFIDCVREKGGKVLVHCEAGISRSPTICMAYLTKTKQFLKFAFYIKORR 297
 OY 106 SCANPNVGFQROLOFE 122
 DB 298 SWVSNFPGFMQLLOYE 314

RESULT 5
 T48906
 protein-tyrosine-phosphatase (EC 3.1.3.48) [imported] - *Chlamydomonas eugametos*

C: Species: *Chlamydomonas eugametos*

C: Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000

C: Accession: T48906

R: Harting, M.A.; Siderius, M.; Joank, C.; Hirt, H.; Walton, K.M.; Musgrave, A.
 Plant J. 7, 981-988, 1995

A: Title: Tyrosine phosphatase signalling in a lower plant: cell-cycle and oxidative

A: Reference number: 225005; MUID: 95323001

A: Accession: T48906

A: Status: preliminary; translated from GB/EMBL/DBDJB

A: Molecule type: mRNA

A: Residues: 1-276 <HAR>

A: Cross-references: EMBL: X77938; NID: g992593; PIDN: CAAS4910.1; PID: g992594

A: Experimental source: strain UTEX 10

C: Genetics:

A: Gene: VHL-PTP13

C: Keywords: phosphoric monoester hydrolase

Query Match 20.6%; Score 185; DB 2; Length 276;
 Best Local Similarity 33.3%; Pred. No. 4.8e-11;
 Matches 52; Conservative 22; Mismatches 52; Indels 30; Gaps 5;

OY 8 ILPG-ILYIGNFKDARDAEQLSKNKYTHILSVHDS-----PGLCWRTTHFKESI----- 54
 DB 90 IVPGLILSSCEVESSLLTKVTHLQGEELKRSHPG---RFTYLSLPTIDMEGQD 146
 OY 55 -----KTHFCRLGSGESCTVHCLAGVSRSVTLVIATYMTVDFGMDALHTVRAGR 105

Db 147 IVALPSCFQLOAQASGVCLVHCLAGISRSASVVIAYLMTQGMPTEARAVRRAR 206
QY 106 SCANPNVGFQROLOEFKEHEVHOYROWLKEEYGS 141
Db 207 SKVYPNTEFTLQLOELRLRESGAIQW-----GDP 237

RESULT 6

149365
protein tyrosine phosphatase - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 149365
R:Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
J. Biol. Chem. 270, 26782-26785, 1995
A:Title: A single mutation converts a novel phosphotyrosine binding domain into a dual-S
A:Reference number: 149364; MUID:96070766
A:Accession: 149365
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-223 <RES>
A:Cross-references: EMBL:U034973; NID:g1063624; PIDN:AAA87037.1; PID:g1063626
C:Genetics:
A:Introns: 168/3
C:Superfamily: VHL-type dual specificity phosphoprotein phosphatase homology
F:36-174/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>

Query Match 20.5%; Score 183.5; DB 2; Length 223;
Best Local Similarity 33.8%; Pred. No. 5.3e-11;
Matches 50; Conservative 18; Mismatches 53; Indels 27; Gaps 3;

QY 1 MGNGMKNKILPGLYIGNFEDARDAEO--LSKNKVTHI----- 34
Db 25 MRREMQEVLPLFLGPIYSSAMSKLPILOKHGITHICIRONIEANFIKPNFQOLFRYL 84
QY 35 LSVHDSPLCWRTRHFKESIKFIHECRLRGESCLVHCLAGVSRVTLVIAYIMTVTDG 94
Db 85 LDIDNP--VENIIRFPMTKEIDGSLONGKVLVHGNAISRSAAFIYATIMETFGMKY 143
QY 95 EDALHTVARGSCANPNVGFQROLOEFE 122
Db 144 RDAFAYVOERRFCINPNAGFVHOLOEYE 171

RESULT 7

T03074
dual specificity phosphoprotein phosphatase homolog - Chilo iridescent virus
C:Species: Chilo iridescent virus
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C:Accession: T03074
R:Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A:Reference number: Z14834; MUID:99114193
A:Accession: T03074
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-142 <BAH>
A:Cross-references: EMBL:AF003534; NID:g2738385; PIDN:AAB94448.1; PID:g2738421

Query Match 20.3%; Score 182; DB 2; Length 142;
Best Local Similarity 31.7%; Pred. No. 4.4e-11;
Matches 44; Conservative 23; Mismatches 52; Indels 20; Gaps 3;

QY 7 KILPGLYGNFEDARDAQLSKNKVTHLSVHDSPL--CWR-----RHFKE 54
Db 5 KIVENLYIGNIONGIRHSNYGFKITINLRFENNOGIPFVWINIDSSSDLYSHLOKVT 64
QY 55 KEIHRCRLRGESCLVHCLAGVSRVTLVIAYIMTVTDGWDALHTVARGSCANPNVGF 114
Db 65 TLIHDSINGKNVLYVHCAGISRSATVIYATIMRSKRYSLDARFVKKRSITFPNAGF 124

QY 115 QROLOEFKEHEVHOYROWL 133
Db 125 IKOLAQFDR-----WL 135

RESULT 8

149364
protein tyrosine phosphatase - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 149364
R:Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
J. Biol. Chem. 270, 26782-26785, 1995
A:Title: A single mutation converts a novel phosphotyrosine binding domain into a du
A:Reference number: 149364; MUID:96070766
A:Accession: 149364
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-205 <RES>
A:Cross-references: EMBL:U034973; NID:g1063624; PIDN:AAA87036.1; PID:g1063625
C:Superfamily: VHL-type dual specificity phosphoprotein phosphatase homology
F:36-174/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>

Query Match 19.3%; Score 173.5; DB 2; Length 205;
Best Local Similarity 30.3%; Pred. No. 4.9e-10;
Matches 53; Conservative 20; Mismatches 61; Indels 41; Gaps 5;

QY 1 MGNGMKNKILPGLYIGNFEDARDAEO--LSKNKVTHI----- 34
Db 25 MRREMQEVLPLFLGPIYSSAMSKLPILOKHGITHICIRONIEANFIKPNFQOLFRYL 84
QY 35 LSVHDSPLCWRTRHFKESIKFIHECRLRGESCLVHCLAGVSRVTLVIAYIMTVTDG 94
Db 85 LDIDNP--VENIIRFPMTKEIDGSLONGKVLVHGNAISRSAAFIYATIMETFGMKY 143
QY 95 EDALHTVARGSCANPNVGFQROLOEFKEHEVHOYROWLKEEYGS---PLDAAE 146
Db 144 RDAFAYVOERRFCINPNAGF-----VHQLQLWLSNNSARSAPLPKQR 187

RESULT 9

S31304
protein-tyrosine-phosphatase (EC 3.1.3.48) YVH1 - yeast (Saccharomyces cerevisiae)
M:Alternate names: protein YIR026c
C:Species: Saccharomyces cerevisiae
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
C:Accession: S31304; S48488; S28650
R:Guan, K.; Hakes, D.J.; Wang, Y.; Park, H.D.; Cooper, T.G.; Dixon, J.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 12175-12179, 1992
A:Title: A yeast protein phosphatase related to the vaccinia virus VHL phosphatase 1
A:Reference number: S31304; MUID:93101690
A:Accession: S31304
A:Molecule type: DNA
A:Residues: 1-364 <GUA>
A:Cross-references: EMBL:L04673; NID:g172167; PIDN:AAA34874.1; PID:g172168

R:Rowley, K.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48478
A:Accession: S48488

A:Molecule type: DNA
A:Residues: 1-364 <ROW>
A:Cross-references: GB:247047; EMBL:Z38061; NID:g603997; PID:g763371; GSPDB:GMD0009;
R:Buckholz, R.G.; Cooper, T.G.
Yeast 7, 913-923, 1991
A:Title: The allantoinase (DAL1) gene of Saccharomyces cerevisiae.

A:Reference number: S28649; MUID:92206070
A:Accession: S28650
A:Molecule type: DNA
A:Residues: 1-67,69-197,'A1' <BUC>
A:Cross-references: EMBL:M69294
C:Genetics:

A:Gene: SGD:YVH1; MIPS:YIR026C
 A:Cross-references: SGD:S0001465; MIPS:YIR026C
 A:Map position: 9R
 C:Superfamily: Saccharomyces protein-tyrosine-phosphatase YVH1, VHL-type dual specificity
 C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:19-171/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>

Query Match 19.0%; Score 170; DB 1; Length 364;
 Best Local Similarity 24.9%; Pred. No. 2.2e-09;
 Matches 51; Conservative 31; Mismatches 65; Indels 58; Gaps 6;

5 MNKILFGLYIGNFKRDARDAEQL-SKNKVTHILSV-----HDSPG 42
 Db 12 VFRILGIVLGGIRPIIDHRLGAEFNTHILSVIKFOYIPEYLIRKGYTIKNIPIDDD 71
 Qy 43 LCKRTHFKESIKFHECRLRGE-----SCLVHCLAGVSRSTLVIAV 85
 Db 72 VYDVLIQYFDETNRFIDQCLFPNEVEYSPRLVDFKKRQKQAVFAHCOAGLSRSFTFIVAY 131
 Qy 86 IMVTDFGWDALHTVRAGSCANPNVGFQROLOEFK-----HEVHOYRGM-LKEEY 137
 Db 132 LMRVGLSLSMAMHAYKKRKPSEYEPNENFEOHLHLEKMGDFVDPNPAYKQWKLQSI 191
 Qy 138 GESP-----LDAAEAAKNI 151
 Db 192 KIDPSSGSELVNSGMEKDESSQDL 216

RESULT 10
 T21380
 hypothetical protein F26A3.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T21380
 R:McMurray, A.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19415
 A:Accession: T21380
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-226 <MIL>
 A:Cross-references: EMBL:Z78419; PIDN:CAB01700.1; GSPDB:GN00019; CESP:F26A3.4
 A:Experimental source: clone F26A3
 C:Genetics:
 A:Gene: CESP:F26A3.4
 A:Map position: 1
 A:Introns: 117/2; 150/3; 186/3

Query Match 18.7%; Score 167.5; DB 2; Length 226;
 Best Local Similarity 28.6%; Pred. No. 2.2e-09;
 Matches 48; Conservative 33; Mismatches 58; Indels 29; Gaps 5;

5 MNKILFGLYIGNFKRDARDAEQLSKNKVTHILSVHD-----SPGLCWTR----- 48
 Db 14 MSEIVPGLFICGV-SALSDEMKKIRTHIINATTEVPLNLSGIQRTKMLEPTPTQY 72
 Qy 49 ---HFKESTIKFHECRLRGESCIVHCLAGVSRSTLVIAVIMVTDFGWDALHTVRAGR 105
 Db 73 IYRPHLELQSDQIQALIALDAGCKVLAHVAGVSRASISICLAFILKYCRNLRKAYHLMKSKR 132
 Qy 106 SCANPNVGFQROLOEFKHEVHOYRGM-LKEEYGESPL-QDAEAAKNI 152
 Db 133 SMVRNPLGFWROLIAYEON-----VKENAGSVRLVRDEAPQOLL 172

RESULT 11
 T16056
 hypothetical protein F13D11.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 23-Mar-2001
 C:Accession: T16056

R:Pulton, L.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid F13D11.
 A:Reference number: S69020
 A:Accession: T16056
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-186 <FNU>
 A:Cross-references: EMBL:U40939; NID:q1072175; PID:q1072176; PIDN:AAA81700.1; CESP:F
 C:Genetics:
 A:Gene: CESP:F13D11.3
 A:Introns: 30/3; 57/3; 85/3; 125/3; 172/3

Query Match 18.3%; Score 164; DB 2; Length 186;
 Best Local Similarity 39.0%; Pred. No. 3.9e-09;
 Matches 30; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

Qy 47 TRHFESIKFHECRLRGESCIVHCLAGVSRSTLVIAVIMVTDFGWDALHTVRAGRS 106
 Db 69 TQFFEVVYKIEDAKQGGHNVITVCAGVSRSATLITVMTENLSLEAYLYQNVYRP 128
 Qy 107 CANPNVGFQROLOEFK 123
 Db 129 IISPNIGFWRMIDFEK 145

RESULT 12
 S29090
 dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 1 - human
 N:Alternate names: protein-tyrosine-phosphatase CL100; protein-tyrosine-phosphatase,
 C:Species: Homo sapiens (man)
 C>Date: 25-Feb-1994 #sequence_revision 02-May-1994 #text_change 11-Jun-1999
 C:Accession: S29090; A53052
 R:Keyse, S.M.; Emslie, E.A.
 Nature 359, 644-647, 1992
 A:Title: Oxidative stress and heat shock induce a human gene encoding a protein-tyro
 A:Reference number: S29090; MUID:93024952
 A:Molecule type: mRNA
 A:Accession: S29090
 A:Residues: 1-367 <KEY>
 A:Cross-references: EMBL:X68277; NID:929980; PIDN:CAAA48338.1; PID:q29981
 R:Kwak, S.P.; Hakes, D.J.; Martell, K.J.; Dixon, J.E.
 J. Biol. Chem. 269, 3596-3604, 1994
 A:Title: Isolation and characterization of a human dual specificity protein-tyrosine
 A:Reference number: A53052; MUID:94148864
 A:Accession: A53052
 A:Molecule type: DNA
 A:Residues: 1-367 <KMA>
 A:Experimental source: Leukocyte
 A:Note: sequence extracted from NCBI backbone (NCBIN:143800, NCBIN:143802, NCBIN:143
 C:Genetics:
 A:Gene: GDB:DU5P1; PTPN10
 A:Cross-references: GDB:136197; OMIM:600714
 A:Map position: 5q34-5q34
 C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specific
 C:Keywords: heat shock; phosphoprotein; phosphoric monoester hydrolase; stress-induc
 F:181-312/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL
 F:258/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:264/Binding site: substrate phosphate (Arg) #status predicted

Query Match 17.9%; Score 161; DB 1; Length 367;
 Best Local Similarity 29.8%; Pred. No. 1.8e-08;
 Matches 42; Conservative 20; Mismatches 53; Indels 26; Gaps 2;

Qy 4 GMNKILFGLYIGNFKRDARDAEQLSKNKVTHILSV-----HDSP 41
 Db 173 GVEILPFLYIGSAVHASRKMDLALITALINSAKPNHFEHGYKRSIPEDNHRKD 232
 Qy 42 GLCKRTHFKESIKFHECRLRGESCIVHCLAGVSRSTLVIAVIMVTDFGWDALHTV 101
 Db 233 ISSW-----FNEAIDPIDSINAGGRVFFVHCAGISRSATICTLAYLMRTNRYKLDAAFEV 288

OY 102 RAGSCAMPNPGFORLOEPE 122
 DB 289 KORRSITSPNFSFMGQLLOFE 309

RESULT 13

T46405
 hypothetical protein DKFZp43401321.1 - human
 C:Species: Homo sapiens (man)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
 C:Accession: T46405
 R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 Submitted to the Protein Sequence Database, January 2000
 A:Reference number: 223034
 A:Accession: T46405
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-303 <AAA>
 A:Cross-references: EMBL:AL137704
 A:Experimental source: adult testis; clone DKFZp43401321
 C:Genetics:
 A:Note: DKFZp43401321.1
 C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity

Query Match 17.7%; Score 159; DB 2; Length 303;
 Best Local Similarity 31.9%; Pred. No. 2.2e-08;
 Matches 46; Conservative 20; Mismatches 46; Indels 32; Gaps 4;

OY 4 GMNKLPLGLYGNFKDADAQSLKKNKYTHLSV-----HDSF 41
 DB 104 GPVELLPGLYGSAYHAARRMDLALGITALLNVSSDCPNHFEHGYQKCIPEVDNHRAD 163
 OY 42 GLCWTRHFKESIKFI---HECRLGEGSLVHCLAGVRSYLVATYMTVTDGEMDAL 98
 DB 164 ISSW---FMEAIETIDAVKDCRGR--VLVHCQGISRSATICTLAYIMMKRRVRLERAF 216
 OY 99 HTVRAGSCAMPNPGFORLOEPE 122
 DB 217 EFVKORRSITSPNFSFMGQLLOFE 240

RESULT 14

A56947
 dual specificity phosphatase (EC 3.1.3.-) HNH2 - rat
 N:Alternate names: mitogen-activated protein kinase phosphatase 2
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Mar-1999
 C:Accession: A56947
 R:Misra-Press, A.; Rim, C.S.; Yao, H.; Roberson, M.S.; Stork, P.J.S.
 J. Biol. Chem. 270, 14587-14596, 1995
 A:Title: A novel mitogen-activated protein kinase phosphatase. Structure, expression, an
 A:Reference number: A56947; MUID:95301550
 A:Accession: A56947
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-393 <MTS>
 C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specificity
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase
 F:202-333/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
 F:279/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:285/Binding site: substrate phosphate (Arg) #status predicted

Query Match 17.7%; Score 159; DB 2; Length 393;
 Best Local Similarity 31.9%; Pred. No. 3e-08;
 Matches 46; Conservative 20; Mismatches 46; Indels 32; Gaps 4;

OY 4 GMNKLPLGLYGNFKDADAQSLKKNKYTHLSV-----HDSF 41
 DB 194 GPVELLPGLYGSAYHAARRMDLALGITALLNVSSDCPNHFEHGYQKCIPEVDNHRAD 253

OY 42 GLCWTRHFKESIKFI---HECRLGEGSLVHCLAGVRSYLVATYMTVTDGEMDAL 98
 DB 254 ISSW---FMEAIETIDAVKDCRGR--VLVHCQGISRSATICTLAYIMMKRRVRLERAF 306
 OY 99 HTVRAGSCAMPNPGFORLOEPE 122
 DB 307 EFVKORRSITSPNFSFMGQLLOFE 330

RESULT 15

A56115
 dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 4 - human
 N:Alternate names: dual specificity phosphatase HNH2
 C:Species: Homo sapiens (man)
 C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 24-Apr-1998
 C:Accession: A56115
 R:Guan, K.L.; Butch, E.
 J. Biol. Chem. 270, 7197-7203, 1995
 A:Title: Isolation and characterization of a novel dual specific phosphatase, HNH2,
 A:Reference number: A56115; MUID:95221370
 A:Accession: A56115
 A:Molecule type: mRNA
 A:Status: preliminary; not compared with conceptual translation
 A:Residues: 1-394 <GUA>
 A:Cross-references: GB:021108
 C:Genetics:
 A:Gene: GDB:DUSP4; HNH2; MKP-2
 A:Cross-references: GDB:433893
 A:Map position: 8p21-8p11.2
 C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHL-type dual specific
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase
 F:203-334/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>
 F:280/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:286/Binding site: substrate phosphate (Arg) #status predicted

Query Match 17.7%; Score 159; DB 2; Length 394;
 Best Local Similarity 31.9%; Pred. No. 3.1e-08;
 Matches 46; Conservative 20; Mismatches 46; Indels 32; Gaps 4;

OY 4 GMNKLPLGLYGNFKDADAQSLKKNKYTHLSV-----HDSF 41
 DB 195 GPVELLPGLYGSAYHAARRMDLALGITALLNVSSDCPNHFEHGYQKCIPEVDNHRAD 254
 OY 42 GLCWTRHFKESIKFI---HECRLGEGSLVHCLAGVRSYLVATYMTVTDGEMDAL 98
 DB 255 ISSW---FMEAIETIDAVKDCRGR--VLVHCQGISRSATICTLAYIMMKRRVRLERAF 307
 OY 99 HTVRAGSCAMPNPGFORLOEPE 122
 DB 308 EFVKORRSITSPNFSFMGQLLOFE 331

Search completed: February 12, 2002, 16:13:32
 Job time: 191 sec

DB 135 GDSITLTPNYLGSQIDSLDETMALDADISVYINLSMTCPSKVCIKEDKNFMRIPVND 194
 QY 47 -----PRHEKSIKFIHECKRLGESCLVHCLAGVSRYTLVAYIMTVDFGMDALHTY 101
 DB 195 YQKSLSYFPMAYEFLEKCRACKCLICHLACLAISSPTLAISYIMKYMKGSDDAVRY 254
 QY 102 RAGSCANPNVGFQROLQEFK-----KHEVQYRQWLK-----DEYGSPL 142
 DB 255 KERRPSISPFNFPMGQLLEVENLIDKHVLDYDQASPHRHMDYGPDDL 304

RESULT 2

DUS9_HUMAN
 ID DUS9_HUMAN STANDARD: PRT: 384 AA.
 AC 099956;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE PHOSPHATASE 4) (MKP-4).
 GN DUSP9 OR MKP4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97184169; PubMed=9030581;
 RA Muda M., Boschart U., Smith A., Antonsom B., Gillion C.,
 RA Chabert C., Camps M., Martin I., Ashworth A., Arltinstall S.;
 RT "Molecular cloning and functional characterization of a novel
 RT mitogen-activated protein kinase phosphatase, MKP-4.";
 RL J. Biol. Chem. 272:5141-5151(1997).
 CC - FUNCTION: INACTIVATES MAP KINASES. HAS A SPECIFICITY FOR THE ERK
 CC FAMILY.
 CC - CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
 CC PROTEIN TYROSINE + PHOSPHATE.
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC - SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.

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 CC -----
 DR EMBL: Y08302; CA69610.1; -.
 DR MIM: 300134; -.
 DR InterPro: IPR000340; DS_phosphatase.
 DR InterPro: IPR001763; Rhodanese_domain.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR Pfam: PF00782; DSPC: 1.
 DR SMART: SM00195; DSPC: 1.
 DR SMART: SM00450; RHOD: 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolyase.
 FT DOMAIN 203 384 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 290 290 BY SIMILARITY.
 FT SEQUENCE 384 AA; 41867 MW; F8598CA95AB379B7 CRC64;

Query Match 23.1%; Score 207; DB 1; Length 384;
 Best Local Similarity 34.9%; Pred. No. 3.7e-14;
 Matches 53; Conservative 22; Mismatches 47; Indels 30; Gaps 3;

QY 7 KILPLIYGNFKARDADQLSKNKVTHILSV-----HDSPL 43

DB 206 QILPNLYLGSARSDANLESLAKIGRIYILNVPNLPNFEKNDPIHYKOIPISDHNSQL 265
 QY 44 CWTRHFKESIKFIHECKRLGESCLVHCLAGVSRYTLVAYIMTVDFGMDALHTY 103
 DB 266 ---SRFPFAIEFIDELSONCGVLVHCLAGVSRYTVAYIMQHLHSLNDADYLVKR 322
 QY 104 GRSCANPNVGFQROLQEFK-----HEVQYRQ 131
 DB 323 KSNISPFNFPMGQLDPERSLRLEHRSQEQ 354

RESULT 3

DUS8_HUMAN
 ID DUS8_HUMAN STANDARD: PRT: 625 AA.
 AC Q13202;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH-5).
 GN DUSP8 OR VHS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=96009533; PubMed=7561881;
 RA Martell K.J., Seasholtz A.F., Kwak S.P., Clemens K.K., Dixon J.E.;
 RA "HVH-5: a protein tyrosine phosphatase abundant in brain that
 RT inactivates mitogen-activated protein kinase.";
 RL J. Neurochem. 65:1823-1833(1995).
 CC - FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
 CC PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
 CC SIMILARITY).
 CC - CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
 CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
 CC - TISSUE SPECIFICITY: ABUNDANT IN BRAIN, HEART, AND SKELETAL MUSCLE.
 CC - SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U27193; AAA83151.1; -.
 DR MIM: 602038; -.
 DR InterPro: IPR000340; DS_phosphatase.
 DR InterPro: IPR002965; P-rich_extensn.
 DR InterPro: IPR001763; Rhodanese_domain.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR Pfam: PF00782; DSPC: 1.
 DR PRINTS: PRO1217; PRICHEXTENS.
 DR SMART: SM00195; DSPC: 1.
 DR SMART: SM00450; RHOD: 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolyase; Nuclear protein.
 FT DOMAIN 28 43 CH2 A DOMAIN.
 FT DOMAIN 117 132 CH2 B DOMAIN.
 FT DOMAIN 162 430 PROTEIN-TYROSINE PHOSPHATASE.
 FT DOMAIN 310 550 PRO-RICH.
 FT ACT_SITE 246 246 BY SIMILARITY.
 FT SEQUENCE 625 AA; 65840 MW; DCBEA14487219666 CRC64;

FT	DOMAIN	162	432		POLY-ARG.	
FT	DOMAIN	452	459		POLY-TYROSINE PHOSPHATASE.	
FT	DOMAIN	555	558		POLY-SER.	
FT	DOMAIN	559	576		POLY-CIT.	
FT	DOMAIN	577	600		POLY-SER.	
FT	DOMAIN	311	552		PRO-RICH.	
FT	ACT SITE	246	246		BY SIMILARITY.	
SQ	SEQUENCE	663 AA;	68847 MW;	416F429A12C1FA7C CRC64;		


```

Query Match      22.7%; Score: 203.5; DB 1; Length 663;
Best Local Similarity 32.4%; Pred. No. 1.7e-13;
Matches 45; Conservative 29; Mismatches 46; Indels 19; Gaps 2;

```

QY 4 GKMKILPGLIYNKRDARDAEQLSKNKVTHLSYHDS---PGLCKRTRHK----- 51
 |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 Db 160 GLRIPLHLHYLGSOKDLNMDLTONGISYLVAINSNCPRKDFCESEFMPIINDNYCE 219
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 QY 52 -----ESTIKFEHCRLRGESCIVHCLAGVSRSVTLYAVIMTYVDGEMDALHTVRAG 104
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 Db 220 KLFPMWKSIEFDIKAKISSCVYIVHCLAGISRSATTAIAIIMTKMSSSDAIRFYKDR 279
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 QY 105 RSCANPNVGFORQLQEPEK 123
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 Db 280 RPSTSPNFNLGCLLEYER 298
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 5
 DUST7_RAT STANDARD; PRT; 280 AA.
 ID DUST7_RAT
 AC 063340;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16)
 DE [DUAL SPECIFICITY PROTEIN PHOSPHATASE MKP-X] (FRAGMENT).
 GN DUSP7 OR MKPX.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STAIN-SPRAGUE-DAWLEY; TISSUE-Neuron;
 RX MEDLINE=96224012; Pubmed=8626780;
 RA Muda M., Boschetti U., Dickinson R., Martinou J.C., Martinou I.,
 RA Camps M., Schlegel W., Arkinstall S.;
 RT "MKP7, a novel cytosolic protein-tyrosine phosphatase that
 RT exemplifies a new class of mitogen-activated protein kinase
 RT phosphatase.";
 RT J. Biol. Chem. 271:4319-4326(1996).
 CC -1. CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
 CC AMINOACID TYROSINE + PHOSPHATE.
 CC -1. SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1. SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
 CC
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 CC
 DR EMBL: X94186; CAA63896.1; -.
 DR HSSP: P51452; IAYR.
 DR InterPro: IPRO00340; DS_phosphatase.
 DR InterPro: IPRO00387; TYR_phosphatase.
 DR Pfam: PF00782; DSPc_1.
 DR SMART: SM00195; DSPc_1.
 DR ProSITE: PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.

DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase.
 FT NON_TER 1 1
 FT ACT_SITE 192 192 BY SIMILARITY.
 SQ SEQUENCE 280 AA; 30668 MW; 45DeF4A92F2BDDF CRC64;

Query Match 22.0%; Score 197; DB 1; Length 280;
 Best Local Similarity 35.0%; Pred. No. 2.8e-13;
 Matches 49; Conservative 22; Mismatches 43; Indels 26; Gaps 2;

QY 7 KILPGYIGNFKDARAEOLSKNKVTHLSV-----HDSPTL 43
 DB 108 QILPYLYLGCADSTNLDVKGKIKYILNVTNLPNAFEGGEFTYKQIPISDHSONL 167
 QY 44 CWRTFHKEKSIKFIHECRLEGESCLVHCLAGVRSVTLVIAYIMTYDGMEDALHTYRA 103
 DB 168 ---SQFFPAISFIDARSKKCGVLVHCLAGISRSVTVVAILMKRMNLSLNDAYDFYKR 224
 QY 104 GRSCANPNVGFQROLOEFK 123
 DB 225 KRSNISPENFMGQLDFEER 244

RESULT 6
 ID DUS7_HUMAN STANDARD; PRT; 322 AA.
 AC Q16829;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (DUAL SPECIFICITY PROTEIN PHOSPHATASE PYST2) (FRAGMENT).
 GN DUSP7 OR PYST2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=96312959; PubMed=8670865;
 RA Groom L.A., Sneddon A.A., Alessi D.R., Dowd S., Keyse S.M.;
 RT "Differential regulation of the MAP, SAP and RK/p38 kinases by Pyst1,
 RL a novel cytosolic dual-specificity phosphatase.";
 EMBO J. 15:3621-3632(1996).
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
 CC PROTEIN TYROSINE + PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
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 CC -----
 CC EMBL: X93921; CA63814.1; -
 DR HSSP: P51452; 1YHR.
 DR MIM: 602749; -
 DR InterPro: IPR000340; DS_phosphatase.
 DR InterPro: IPR000387; TYR_phosphatase.
 DR Pfam: PF00782; DSPC; 1.
 DR SMART: SM00195; DSPC; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
 KW Hydrolase.
 FT NON_TER 1 1
 FT ACT_SITE 234 234 BY SIMILARITY.

SQ SEQUENCE 322 AA; 35449 MW; E89B1C2ABB2E75DE CRC64;

Query Match 22.0%; Score 197; DB 1; Length 322;
 Best Local Similarity 35.0%; Pred. No. 3.3e-13;
 Matches 49; Conservative 22; Mismatches 43; Indels 26; Gaps 2;

QY 7 KILPGYIGNFKDARAEOLSKNKVTHLSV-----HDSPTL 43
 DB 150 QILPYLYLGCADSTNLDVKGKIKYILNVTNLPNAFEGGEFTYKQIPISDHSONL 209
 QY 44 CWRTFHKEKSIKFIHECRLEGESCLVHCLAGVRSVTLVIAYIMTYDGMEDALHTYRA 103
 DB 210 ---SQFFPAISFIDARSKKCGVLVHCLAGISRSVTVVAILMKRMNLSLNDAYDFYKR 266
 QY 104 GRSCANPNVGFQROLOEFK 123
 DB 267 KRSNISPENFMGQLDFEER 286

RESULT 7
 ID DUS6_HUMAN STANDARD; PRT; 381 AA.
 AC Q16828;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.48) (EC 3.1.3.16)
 DE (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 3) (MAP KINASE
 DE PHOSPHATASE 3) (MKP-3) (DUAL SPECIFICITY PROTEIN PHOSPHATASE PYST1).
 GN DUSP6 OR PYST1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Foreskin;
 RX MEDLINE=96312959; PubMed=8670865;
 RA Groom L.A., Sneddon A.A., Alessi D.R., Dowd S., Keyse S.M.;
 RT "Differential regulation of the MAP, SAP and RK/p38 kinases by Pyst1,
 RL a novel cytosolic dual-specificity phosphatase.";
 EMBO J. 15:3621-3632(1996).
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
 CC PROTEIN TYROSINE + PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
 CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
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RT	"A novel cytoplasmic dual specificity protein tyrosine phosphatase implicated in muscle and neuronal differentiation.";			
RL	J. Biol. Chem. 271:3795-3802(1996).			
CC	-1- FUNCTION: INACTIVATES MAP KINASES. HAS A SPECIFICITY FOR THE ERK FAMILY. IMPLICATED IN MUSCLE AND NEURONAL DIFFERENTIATION.			
CC	-1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + PHOSPHATE.			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; X94185; CAAG3895.1; -;			
DR	EMBL; U42627; AAB06202.1; -;			
DR	HSSP; P51452; 1VHR.			
DR	InterPro; IPR000340; DS_phosphatase.			
DR	InterPro; IPR001763; Rhodanese_domain.			
DR	InterPro; IPR000387; TYR_phosphatase.			
DR	Pfam; PF00782; DSPc; 1.			
DR	Pfam; PF00581; Rhodanese; 1.			
DR	SMART; SM00195; DSPc; 1.			
DR	SMART; SM00450; RHOD; 1.			
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.			
DR	PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.			
DR	PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.			
KW	Hydrolase.			
FT	DOMAIN 206 381			
FT	ACT_SITE 293 293			
SO	SEQUENCE 381 AA; 42318 MW; C311ED0CB6F2888 CMC64;			
		PROTEIN-TYROSINE PHOSPHATASE.		
		BY SIMILARITY.		

	Query Match	21.9%; Score 196; DB 1; Length 381;		
	Best Local Similarity	35.2%; Pred. No. 5,2e-13;		
	Matches 50; Conservative 24; Mismatches 38; Indels 30; Gaps 4;			
QY	7 KILPELYIGNRKDAADAQOLSKNKYTHLSV-----HDSPECL 43			
DB	209 ELPEPLYGCAKDSINLVLVEFGIKYILNVPNLPNLEFNAGEFRYKQIPISDHMSQNL 268			
QY	44 CWRTRHFKESIKETIECHRLRGESC--LVHCLAGVRSRYTVAYITMTQDFGMDALHTY 101			
DB	269 ---SQEFPEALSIDDEA--RGKNGCVLVHCLAGISRSYTVAYVAMQKINLSMNDAYDVI 323			
QY	102 RAGRSCANPNVGFQROLQEFK 123			
DB	324 KMKKSNISPNFNMGQLDFFER 345			
RESULT	9			
DUS5_HUMAN				
ID	DUS5_HUMAN	STANDARD:	PRT:	384 AA.
AC	Q16690; O12997;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16)			
DE	(DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3).			
GN	DUSP5 OR VH3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
TX	TISSUE=Placenta;			
TX	MEDLINE=95138103; PubMed=7836374;			

RA Kwak S.P., Dixon J.E.;
RT "Multiple dual specificity protein tyrosine phosphatases are
RT expressed and regulated differentially in liver cell lines."
RL J. Biol. Chem. 270:1156-1160(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=95050849; PubMed=7961985;
RA Ishibashi T., Bottaro D.P., Michieli P., Kelley C.A.,
RA Aaronson S.A.;
RT "A novel dual specificity phosphatase induced by serum stimulation
RT and heat shock."
RL J. Biol. Chem. 269:29897-29902(1994).
RN [3]
RP REVISIONS.
RA Bottaro D.P.;
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: DISPLAYS PHOSPHATASE ACTIVITY TOWARD SEVERAL SUBSTRATES.
CC THE HIGHEST RELATIVE ACTIVITY IS TOWARD ERK1.
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U16996; AAB06261.1; -
DR EMBL: U15932; AAB64693.2; -
DR HSSP: P51452; 1VHR.
DR MIM: 603069; -
DR InterPro: IPR000340; DS-phosphatase.
DR InterPro: IPR001763; Rhodanese domain.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00782; DSPC; 1.
DR Pfam: PF00581; Rhodanese; 1.
DR SMART: SM00195; DSPC; 1.
DR SMART: SM00450; RHOD; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS0056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolyase; Nuclear protein.
FT DOMAIN 24 39
FT DOMAIN 53 74
FT DOMAIN 79 82
FT DOMAIN 120 135
FT DOMAIN 180 384
FT ACI_SITE 263
FT ACI_SITE 263
FT CONFLICT 9 11
FT CONFLICT 71 71
FT CONFLICT 105 106
SQ SEQUENCE 384 AA; 42107 MW; D2B726F7C0414306 CRC64;

Query Match 20.7%; Score 186; DB 1; Length 384;
Best Local Similarity 33.6%; Pred. No. 5.8e-12;
Matches 46; Conservative 21; Mismatches 52; Indels 18; Gaps 1;

OY 4 GNMKILPLGYIGNFKDADAQLSKNKVTHTLSVHDSGLCWRR----- 48
DB 178 GPVELLPPLYLGSAYHASKCEFLNHTITALINVSRRSTSEACMTHLHKWIPVEDSHRAD 237

OY 49 ---HFKESEIKFTHECRVLGECVAGSVSTVLTATYITDPEGMALHTVRAGR 105
DB 238 ISSHQEALIDFTDVKREKGVLVHCEGIGSRPTICMAYIMKTKQFLKEAFDYIKOR 297
OY 106 SCANPNVGFQROLOEFE 122

DB 298 SMVSPNFGFMQGLQYE 314
ID 1 :||| 11 :||
DUS5_RAT
ID DUS5_RAT STANDARD; PRT; 384 AA.
AC O54838;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16)
DE (MAP-KINASE PHOSPHATASE CPG21).
GN DUSP5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SVRAIN-WISTAR;
RX MEDLINE=96364306; PubMed=9699150;
RA Heyvont D., Ratner A., Bundman M., Lederfein D., Gabarrah A.,
RA Mangelus M., Silverman M.A., Kedar H., Naor C., Kornuc M., Hancock T.,
RA Seger R., Theill L.E., Nedivi E., Richter-Levin G., Citri Y.;
RT "Hippocampal plasticity involves extensive gene induction and multiple
RT cellular mechanisms."
RL J. Mol. Neurosci. 10:75-98(1998).
CC -!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
CC PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
CC PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -!- SIMILARITY: CONTAINS THE CDC25 HOMOLOGY DOMAINS 2 A AND B (CH2
CC DOMAINS A AND B).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF013144; AAB94858.1; -
DR InterPro: IPR000340; DS-phosphatase.
DR InterPro: IPR001763; Rhodanese domain.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00782; DSPC; 1.
DR Pfam: PF00581; Rhodanese; 1.
DR SMART: SM00195; DSPC; 1.
DR SMART: SM00450; RHOD; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolyase; Nuclear protein.
FT DOMAIN 24 39
FT DOMAIN 53 74
FT DOMAIN 79 82
FT DOMAIN 120 135
FT DOMAIN 180 384
FT ACI_SITE 263
FT ACI_SITE 263
SQ SEQUENCE 384 AA; 42094 MW; 56440698BD348700 CRC64;

Query Match 20.7%; Score 186; DB 1; Length 384;
Best Local Similarity 34.3%; Pred. No. 5.8e-12;
Matches 47; Conservative 19; Mismatches 53; Indels 18; Gaps 1;

OY 4 GNMKILPLGYIGNFKDADAQLSKNKVTHTLSVHDSGLCWRR----- 48

D6		178	GPAVLPLFLVLYGSAYHNSKCEFLANLHTPLLANSRRSEACTHLHKYMPIVEDSHFAD	237
Oy	---	49	--HFESIKATIHCCRLGSCGLVHCAGVSRSVTIVIAITMYTDFGWEDALHTYAGR	105
D6		238	ISSHHOELIDFDICVREBGGKVLVHCAGVSRSPTICMAYIMKTOKPFRLEKAFFIYIKOR	297
Oy		106	SCANPNVGFOROLOEFE	122
D6		298	SWSNFGFMGLLOYE	314
		RESULT	11	
P	PP3_	CHELU		
ID	PP3_CHELU	STANDARD;	PRU;	276 AA.
AC	Q39491;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	DUAL SPECIFICITY PROTEIN PHOSPHATASE (EC 3.1.3.48) (EC 3.1.3.16).			
GN	VH-PP313..			
OS	Chlamydomonas eugametos.			
OC	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;			
OC	Chlamydomonadaceae; Chlamydomonas.			
OX	NCBI_TaxID=3053;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
KC	STRAIN-UTEX 10;			
RX	MEDLINE=95323001; Pubmed=7599654;			
RA	Harting M.A., Siderius M., Jonak C., Hirt H., Walton K.M.,			
RA	Musgrave A.;			
RT	"Tyrosine phosphatase signalling in a lower plant: cell-cycle and			
RT	oxidative stress-regulated expression of the Chlamydomonas eugametos			
RT	vih-pp313 gene."			
RL	Plant J. 7:961-988(1995).			
CC	-1- FUNCTION: COULD BE INVOLVED IN TYROSINE PHOSPHATASE SIGNALLING			
CC	PATHWAYS, HAVING MAP-KINASES AS SUBSTRATES.			
CC	-1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =			
CC	PROTEIN TYROSINE + ORTHOPHOSPHATE.			
CC	-1- DEVELOPMENTAL STAGE: NONDIVIDING GAMETES DID NOT EXPRESS THE VH-			
CC	PPP13 GENE WHEREAS SYNCHRONOUSLY DIVIDING VEGETATIVE CELLS ONLY			
CC	EXPRESSED VIH-PPP13 IN THE EARLY G1-PHASE OF THE CYCLE.			
CC	-1- INDUCTION: BY OXIDATIVE STRESS.			
CC	-1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-			
CC	TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUPERFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X77938; CAAS4910.1; .			
DR	HSSP; P51452; IAVR.			
DR	InterPro: IPRO000340; DS_phosphatase.			
DR	InterPro: IPRO000387; TYR_phosphatase.			
DR	pfam; PF00782; DSPc; 1.			
DR	SMART; SM00195; DSPe; 1.			
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.			
DR	PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.			
KM	Hydrolase.			
FT	DOMAIN	89	276	CATALYTIC.
FT	ACT_SITE	172	172	
FT	MUTAGEN	172	172	C->S; INACTIVE.
SQ	SEQUENCE	276 AA;	30310 MM;	034EE63951EO3381 CRC64;

Query Match	20.6%	Score 185;	DB 1;	length 276;
Best Local Similarity	33.3%	Pred. No. 5e-12;		
Matches	52;	Conservative	22;	Mismatches 52;
				Indels 30;
				Gaps 5;

```

QY      8 ILPG-LYIYGNKARADQGLSKNNVHTILSYHOS-----PGLMQRTHFEESI-----54
Dd      90 IVPKLLISSEVEESESLLKLGVTHTILVQGEELKPSHG--RPTYSLLPIIDNEGQ 146
QY      55 -----KPIHCRIKRGESCITHCACAGSRSVTLVATIMTYIDRGEDALHTVRAGR 105
Dd      147 IVALLPSCFOPLQQAQASGGVCLVHCILAGISRSASVATILMTQCMPTEARAMVRAR 206
QY      106 SCANPNVGFQFOLQEFKHEHVOYRMKLKEEGSP 141
Dd      207 SKVYPNMGFTIQLQDELRLKRESAIGM-----GDPF 237

```

RESULT	12
PROTEIN	12
PROTEIN_ID	PROTEIN_YEAST
STANDARD	PROT
364 AA	
002256;	
01-OCT-1993 (Rel. 27, Created)	
01-OCT-1993 (Rel. 27, Last sequence update)	
01-NOV-1997 (Rel. 35, Last annotation update)	
PROTEIN-TYROSINE PHOSPHATASE YVH1 (EC 3.1.3.48) (PTPASE YVH1).	
YVH1 OR Y1R026C.	
Saccharomyces cerevisiae (Baker's yeast).	
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	
Saccharomycetales; Saccharomycetaceae; Saccharomyces.	
NCBI_TaxID=4932;	
SEQUENCE FROM N.A.	
MEDLINE=93101690; PubMed=1334559;	
Guan K., Hakes D.J., Wang Y., Park H.-D., Cooper T.G., Dixon J.E.;	
"A yeast protein phosphatase related to the vaccinia virus VHL	
phosphatase is induced by nitrogen starvation";	
Proc. Natl. Acad. Sci. U.S.A. 89:12175-12179(1992).	
[2]	
SEQUENCE FROM N.A.	
STRAIN=5288C / AB972;	
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,	
Churcher C.M., Connor R., Copley T., Dear S., Devlin K., Fraser A.,	
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,	
Louis E., Lyne G., Moule S., Moule T., Odell C., Pearson D.,	
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,	
Walsh S.V., Whitehead S.;	
Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.	
[3]	
SEQUENCE OF 1-197 FROM N.A.	
MEDLINE=92206070; PubMed=1803816;	
Buckholz R.G., Cooper T.G.;	
"The allantoinase (DAL1) gene of Saccharomyces cerevisiae.";	
Yeast 7:913-923(1991).	
[4]	
ERRATUM.	
Buckholz R.G., Cooper T.G.;	
Yeast 8:239-239(1992).	
[5]	
SIMILARITY TO VHL.	
MEDLINE=93174465; PubMed=8438236;	
Guan K., Hakes D.J., Dixon J.E., Park H.D., Cooper T.G.;	
"The yeast open reading frame encoding a dual specificity	
phosphatase.";	
Trends Biochem. Sci. 18:6-6(1993).	
-I- FUNCTION: MAY BE DIRECTLY INVOLVED IN SIGNAL TRANSDUCTION AND/OR	
CELL CYCLE REGULATION. IT IS NECESSARY FOR MAINTAINING GROWTH RATE	
OR SPORE GERMINATION. COULD SHOW BOTH ACTIVITY TOWARD TYROSINE-	
PROTEIN PHOSPHATE AS WELL AS WITH SERINE-PROTEIN PHOSPHATE.	
-I- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =	
PROTEIN TYROSINE + ORTHOPHOSPHATE.	
-I- INDUCTION: BY NITROGEN STARVATION.	
-I- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-	
TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.	

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DR EMBL; L04673; AAA34874.1; -;
DR EMBL; Z38061; CAA86186.1; -;
DR EMBL; M69294; -; NOT_ANNOTATED_CDS.
DR PIR; S31304; S31304.
DR PIR; S28650; S28650.
DR PIR; S48488; S48488.
DR SGB; S0001465; YVH1.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolyase.
FT DOMAIN 1 172 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 117 117 BY SIMILARITY.
FT CONFLICT 71 71 MISSING (IN REF. 3).
SQ SEQUENCE 364 AA; 41185 MW; 9E75C7C14353B43 CRC64;

Query Match 19.0%; Score 170; DB 1; Length 364;
Best Local Similarity 24.9%; Pred. No. 2.6e-10;
Matches 51; Conservative 31; Mismatches 65; Indels 58; Gaps 6;

QY 5 NKKILPGLYIGNFKDARDAEQLSKNKVTHILSV-----HDSPG 42
D 12 VTRILGGLYIGIRIIDHRLPGAENFTHILSVIKFOYIPRYLLRKGTLLKNIPIDDD 71
QY 43 LCMRTFRKESIKFTHECLRGE-----SCLVHCLAGVSRVTLVIAY 85
D 72 VTDVLYQYEDETNRKFDQCLFNEVEYSPRLVDFKPKKPGQGAFAVHCQAGLSRVTFIYAY 131
QY 86 IMTVDFPQMEDALHTVRGRSCANPNVGFQROLOEFK-----HEVHQYQOM-LKKEY 137
D 132 LMYRGISLSMAMHAAVKKRKSVEPENNEMQDLHFERKMGDFDPDNPAYKQMKLOSI 191
QY 138 GESP-----LQDAEAKNI 151
D 192 KLDPSGSELVNSGMFKDSESSQDL 216

RESULT 13
DUSC_HUMAN STANDARD; PRT; 340 AA.
AC 09UN16;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DUAL SPECIFICITY PROTEIN PHOSPHATASE 12 (EC 3.1.3.48) (EC 3.1.3.16)
DE (DUAL-SPECIFICITY TYROSINE PHOSPHATASE YVH1).
GN DUSP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RX MEDLINE=99377030; PubMed=10446167;
RA Mada M., Manning E.R., Orth K., Dixon J.E.;
RT "Identification of the human YVH1 protein-tyrosine phosphatase
orthologue reveals a novel zinc binding domain essential for in vivo
function.";
RT J. Biol. Chem. 274:23991-23995(1999).
CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
CC PROTEIN TYROSINE + PHOSPHATE.
CC -1- COFACTOR: BINDS 2 MOLES OF ZINC PER MOLE OF PROTEIN.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST EXPRESSION IN SPLEEN,
CC TESTIS, OVARY, AND PERIPHERAL BLOOD LEUKOCYTES AND LOWER
CC EXPRESSION IN LIVER AND LUNG.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.

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DR EMBL; AF119226; AAD51134.1; -;
DR MIM; 604835; -;
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; UNKNOWN_1.
KW Hydrolyase; Zinc; Metal-binding.
FT ACT_SITE 115 115 BY SIMILARITY.
FT CONFLICT 115 115
SQ SEQUENCE 340 AA; 37687 MW; 56B52192B42C73EB CRC64;

Query Match 18.7%; Score 168; DB 1; Length 340;
Best Local Similarity 29.3%; Pred. No. 3.8e-10;
Matches 49; Conservative 27; Mismatches 59; Indels 32; Gaps 6;

QY 5 NKKILPGLYIGNFKDARDAEQLSKNKVTHILSVHD-----SPGL-CWR----- 46
D 27 MEVQPGLYFGCAAAVAEPDHLREAGITAVLVDSPEPSFKAGPVEDMLRFVADLKP 86
QY 47 ----TRHRESIKFTHECLRGESCIYHCLAGVSNVTLVIAYIMTVDFPQMEDALHTVR 102
D 87 ETDLSLHSDRCVAFIFGOAAEGRVAVLVHCHAGVSRSAVITAFLLKKTQDLPEKAYEKIQ 146
QY 103 AGRSCANPNVGFQROLOEFK--HEV-----HGYR-OMLKEEYGE 139
D 147 ILKPKAKNKEGFEMQKLQAMGYEVDISSAIYKQRLQKTEKYEP 193

RESULT 14
DUSL_HUMAN STANDARD; PRT; 367 AA.
AC P28562;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DUAL SPECIFICITY PROTEIN PHOSPHATASE 1 (EC 3.1.3.48) (EC 3.1.3.16)
DE (MAP KINASE PHOSPHATASE-1) (MKP-1) (PROTEIN-TYROSINE PHOSPHATASE
CL100) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH1).
GN DUSP1 OR PTPN10 OR MKP1 OR VHI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-ForeSkin; PubMed=1406996;
RA Keyes S.M., Emslie E.A.;
RT "Oxidative stress and heat shock induce a human gene encoding a
RT protein-tyrosine phosphatase.";
RT Nature 359:644-647(1992).
CC -1- FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP
CC KINASE ERK2 ON BOTH THR-183 AND TYR-185.

CC	-1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =	
CC	PROTEIN TYROSINE + ORTHOPHOSPHATE.	
CC	-1- INDUCTION: BY OXIDATIVE STRESS AND HEAT SHOCK.	
CC	-1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-	
CC	TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
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CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.1sb-slb.ch/announce/	
CC	or send an email to license@1sb-slb.ch).	
CC	-----	
DR	EMBL, X68277, CAA48338.1, -. .	
DR	PIR: S29090; S29090.	
DR	HSSP: P51452; 1VHR.	
DR	MIM: 600714; .	
DR	InterPro: IPR000340; .DS phosphatase.	
DR	InterPro: IPR001763; Rhodanese_domain.	
DR	InterPro: IPR000387; TYR_phosphatase.	
DR	Pfam: PF00782; DSPc; 1.	
DR	Pfam: PF00581; Rhodanese; 1.	
DR	SMART: SM00195; DSPc; 1.	
DR	SMART: SM00450; RHOD; 1.	
DR	PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.	
DR	PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.	
DR	PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.	
KW	Hydrolase; Cell cycle.	
FT	DOMAIN 175 367	
FT	ACT SITE 258	
SO	SEQUENCE 367 AA; 39297 MW; 11BDID39A9FCD51F CRC64;	
	PROTEIN-TYROSINE PHOSPHATASE.	
	BY SIMILARITY	

Query Match	17.9%	Score 161;	DB 1;	Length 367;
Best Local Similarity	29.8%	Pred. No. 2	3e-09;	
Matches 42;	Conservative 20;	Mismatches 53;	Indels 26;	Gaps 2

[illegible]

RESULT	15
DUS4_HUMAN	
ID	DUS4_HUMAN
AC	Q13115;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	DUAL SPECIFICITY PROTEIN PHOSPHATASE 4 (EC 3.1.3.48) (EC 3.1.3.16)
DE	(DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH2).
GN	DUSP4 OR VH2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RP	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=95221370; PubMed=7535768;
RA	Guan K.-L., Butch E.;
RT	"Isolation and characterization of a novel dual specific phosphatase
RT	HVH2, which selectively dephosphorylates the mitogen-activated
RT	protein kinase.";
RL	J. Biol. Chem. 270:7197-7203(1995).

```

CC      -1- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
CC      DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
CC      ERK1 AND ERK2.
CC      -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O =
CC      PROTEIN TYROSINE + ORTHOPHOSPHATE.
CC      -1- SUBCELLULAR LOCATION: NUCLEUS.
CC      -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC      TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U21108; AAA85119.1; -.
DR      HSSP; P51452; 1VHR.
DR      MIM; 602747; -.
DR      InterPro: IPR000340; DS_phosphatase.
DR      InterPro: IPR001763; Rhodanese_domain.
DR      InterPro: IPR000387; TYR_phosphatase.
DR      Pfam; PF00782; DSPc; 1.
DR      Pfam; PF00581; Rhodanese; 1.
DR      SMART; SM00195; DSPc; 1.
DR      SMART; SM00450; RHOD; 1.
DR      PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR      PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
DR      PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW      Hydrolyase; Nuclear protein.
FT      DOMAIN 46 61
FT      DOMAIN 138 153 CH2 A DOMAIN.
FT      DOMAIN 197 394 CH2 B DOMAIN.
FT      ACT_SITE 280 280 PROTEIN-TYROSINE PHOSPHATASE.
FT      BY_SIMILARITY BY SIMILARITY
SO      SEQUENCE 394 AA; 42953 MW; 0603971759B6952E CRC64;

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Query Match	17.7%	Score 159	DB 1	length 394
Best Local Similarity	31.9%	Pred. NO. 4e-09		
Matches	46	Conservative	20	Mismatches 46; Indels 32; Gaps 4

[illegible]

Search completed: February 12, 2002, 16:15:57
Job time: 181 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2002, 16:13:16 ; Search time 23.64 Seconds

(without alignments)
1033.311 Million cell updates/sec

Title: US-09-544-525-2

Sequence: 1 MGNMKNKILPGIYGNFKDA.....AKNIIAAGCITLKFMAFLRL 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_podent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	831.5	92.7	184	4 Q9NRW4	Q9NRW4 homo sapien
2	791.5	88.2	184	11 Q9NR11	Q9NR11 mus musculu
3	404.5	45.1	275	4 Q9H1R2	Q9H1R2 homo sapien
4	389.5	43.4	608	5 Q9V080	Q9V080 drosophila
5	210	23.4	177	11 Q9CSL5	Q9CSL5 mus musculu
6	210	23.4	482	4 Q9Y6W6	Q9Y6W6 homo sapien
7	210	23.4	483	11 Q9ESS0	Q9ESS0 mus musculu
8	210	23.4	483	11 Q9CZY9	Q9CZY9 mus musculu
9	208.5	23.2	221	5 Q9TY00	Q9TY00 caenorhabdi
10	207	23.1	167	10 Q9M8K7	Q9M8K7 arabidopsi
11	205	22.9	198	10 Q9ZK37	Q9ZK37 arabidopsi
12	205	22.9	198	10 Q9LUG6	Q9LUG6 arabidopsi
13	202	22.5	330	3 Q13632	Q13632 schizosacch
14	199	22.2	378	13 Q91663	Q91663 xenopus lae
15	199	22.2	436	11 Q916C2	Q916C2 mus musculu
16	196	21.9	381	4 Q9BSH6	Q9BSH6 homo sapien
17	196	21.9	381	11 Q9D7L4	Q9D7L4 mus musculu
18	196	21.9	381	11 Q9DBB1	Q9DBB1 mus musculu
19	194.5	21.7	348	5 Q9YVW4	Q9YVW4 drosophila

20	194	21.6	365	5 Q44128	Q44128 caenorhabdi
21	187	20.8	661	10 Q9ATY4	Q9ATY4 zea mays (m
22	186.5	20.8	665	4 Q9BY84	Q9BY84 homo sapien
23	186.5	20.8	690	4 Q9C0G3	Q9C0G3 homo sapien
24	186	20.7	1045	5 Q9NXY1	Q9NXY1 drosophila
25	185.5	20.7	203	5 Q9NG11	Q9NG11 drosophila
26	185.5	20.7	677	11 Q9NMG6	Q9NMG6 mus musculu
27	183.5	20.5	223	11 Q60970	Q60970 mus musculu
28	183.5	20.5	223	11 Q9DCF8	Q9DCF8 mus musculu
29	182	20.3	142	12 Q55737	Q55737 chilo iride
30	181.5	20.2	198	11 Q9D700	Q9D700 mus musculu
31	176.5	19.7	339	11 Q9JTM4	Q9JTM4 rattus norv
32	175	19.5	220	11 Q9N912	Q9N912 mus musculu
33	175	19.5	784	10 Q9C5S1	Q9C5S1 arabidopsi
34	174.5	19.5	211	4 Q9BV47	Q9BV47 homo sapien
35	173.5	19.3	205	11 Q60969	Q60969 mus musculu
36	172	19.2	220	11 Q9D6P6	Q9D6P6 mus musculu
37	172	19.2	476	5 Q9VHV8	Q9VHV8 drosophila
38	172	19.2	738	4 Q9P2P8	Q9P2P8 homo sapien
39	170.5	19.0	140	4 Q9H925	Q9H925 homo sapien
40	167.5	18.7	226	5 Q93592	Q93592 caenorhabdi
41	167	18.6	476	5 Q46122	Q46122 drosophila
42	167	18.6	885	5 Q9BHY8	Q9BHY8 leishmania
43	165.5	18.5	235	4 Q75109	Q75109 homo sapien
44	164	18.3	186	5 Q19388	Q19388 caenorhabdi
45	163.5	18.2	185	11 Q9D7X3	Q9D7X3 mus musculu

ALIGNMENTS

RESULT	1	PRELIMINARY	PRT	184 AA.
Q9NRW4	Q9NRW4	Q9NRW4	Q9NRW4	Q9NRW4
AC	Q9NRW4	Q9NRW4	Q9NRW4	Q9NRW4
DT	01-OCT-2000 (TREMblrel. 15, Created)			
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)			
DT	01-JUN-2001 (TREMblrel. 17, Last annotation update)			
DE	MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE X.			
GN	KRPX.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Gu J., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J.,			
RA	Tu Y., Gu W., Fu G., Huang C.;			
RT	"Novel genes expressed in hematopoietic stem/progenitor cells from			
RT	Myelodysplastic Syndromes patient.";			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF165519; AAF6649.1; -			
DR	InterPro: IPR000340; DS_phosphatase.			
DR	InterPro: IPR000387; TYR_phosphatase.			
DR	Pfam: PF00782; DSPc; 1.			
DR	SMART: SM00195; DSPc; 1.			
DR	PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.			
DR	PROSITE: PS00054; TYR_PHOSPHATASE_DUAL; 1.			
DR	kinase.			
SO	SEQUENCE 184 AA; 20910 MW; B3F962A087C2BA20 CRC64;			
Query Match	92.7%; Score 831.5; DB 4; Length 184;			
Best Local Similarity	88.6%; Pred. No. 4.2e-80;			
Matches	163; Conservative 0; Mismatches 4; Indels 17; Gaps 2;			
QY	1 MGNMKNKILPGIYGNFKDAQDAEQLSKNKVTHILSVHDSFG-----LCW-----45			
Db	1 MGNMKNKILPGIYGNFKDAQDAEQLSKNKVTHILSVHDSAPMLEGVKYLICIPADSPS 60			
QY	46 --RTHEKESIKFTHECRSGSCVHCLAGSRSVTLVIAIKMTVTFQGWDAHLTVRA 103			
Db	61 ONLTHREKESIKFTHECRSGSCVHCLAGSRSVTLVIAIKMTVTFQGWDAHLTVRA 120			

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QY 104 GRSCANPVNGFORLOEFKEKHEVHOYROWLKEEGESPLDAAEAKNLLAAGILKFMF 163
DB 121 GRSCANPVNGFORLOEFKEKHEVHOYROWLKEEGESPLDAAEAKNLLAAGILKFMF 180

QY 164 LRRL 167
DB 181 LRRL 184

RESULT 2
Q99N11 PRELIMINARY; PRT; 184 AA.
AC 099N11:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE DUAL SPECIFICITY PHOSPHATASE TS-DSP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Aoyama K., Matsuda T., Aoki N.;
RT "Molecular cloning of a novel dual specificity phosphatase TS-DSP2.";
DR EMBL; AF237619; AAK15038.1;
SQ SEQUENCE 184 AA: 20997 MW: 64953325E8AB577 CRC64;

Query Match 88.2%; Score 791.5; DB 11; Length 184;
Best Local Similarity 82.6%; Pred. No. 7.1e-76;
Matches 152; Conservative 11; Mismatches 4; Indels 17; Gaps 2;

QY 1 MGNGMKNKILPGIYIGNFKDARDAEQLSKNKVTHLSVHDSFG-----LCW----- 45
DB 1 MGSGMSQILPGIYIGNFKDARDAEQLSKNKVTHLSVHDTARPMLEGVKYLITPADRPS 60
QY 46 --RTHFESIKFIHECKLRGESCCLVHCLAGYSRSVTLYIATIMVTDFGWDALHTYRA 103
DB 61 QNLTFRHFESIKFIHECKLRGESCCLVHCLAGYSRSVTLYIATIMVTDFGWDALHTYRA 120
QY 104 GRSCANPVNGFORLOEFKEKHEVHOYROWLKEEGESPLDAAEAKNLLAAGILKFMF 163
DB 121 GRSCANPVNGFORLOEFKEKHEVHOYROWLKEEGESPLDAAEAKNLLAAGILKFMF 180

QY 164 LRRL 167
DB 181 LRRL 184

RESULT 3
Q9H1R2 PRELIMINARY; PRT; 275 AA.
AC 09H1R2:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BA243J16.6 (NOVEL PROTEIN) (FRAGMENT).
GN BA243J16.6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown A.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL160115; CAC10008.1;
DR InterPro; IPR000340; DS_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.

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DR PROSITE; PS0054; TYR_PHOSPHATASE_DUAL; 1.
FT NON TER 1
SQ SEQUENCE 275 AA: 30129 MW: E1F480D6BD3D3F59 CRC64;

Query Match 45.1%; Score 404.5; DB 4; Length 275;
Best Local Similarity 43.5%; Pred. No. 9.7e-35;
Matches 80; Conservative 26; Mismatches 39; Indels 39; Gaps 3;

QY 1 MGNGMKNKILPGIYIGNF-----KDARDAEQLSKNKVTHLSVHDSFGLCW 45
DB 33 MGNGMTKVLPGIYIGNFIGNFHPASQIGSSILFLSDAKDLDQIGRNKITHLSIHESPOPLL 92
QY 46 R-----TRHFESIKFIHECKLRGESCCLVHCLAGYSRSVTLYIATIMT 88
DB 93 QITTLRLPVDATPEVPIKKHKECINFHCRLNGKGLVC-----TITVATYVMT 145

QY 89 VTFGWDALHTVRAGSCANPVNGFORLOEFKEKHEVHOYROWLKEEGESPLDAAERA 148
DB 146 VTGLGMDVLEAIKATRPANPNPGRQOLEFGNASSQKLRQLEERGESPFRDEEL 205

QY 149 KNIL 152
DB 206 RALL 209

RESULT 4
Q9VU80 PRELIMINARY; PRT; 608 AA.
AC 09VU80:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CG10089 PROTEIN.
GN CG10089.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Gelinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.D., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Peltman G.S., Pan S., Plessner J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaert
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

DR	Pfam; PF00581; Rhodanese; 1.
DR	SMART; SM00195; DSPc; 1.

[illegible]

DR PROSITE: PS50056; TYR_PHOSPHATASE.2; 1.
DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 198 AA; 22017 MW; EBFIC98A17E6450 CRC64;

Query Match 22.9%; Score 205; DB 10; Length 198;
Best Local Similarity 37.8%; Pred. No. 8.2e-14;
Matches 51; Conservative 14; Mismatches 44; Indels 26; Gaps 2;

QY 11 GLYIGNEFKDARDADQLSKNKVTHILSVHDSFGLCWRTH----- 49
DQ 57 GLYIGSVAAASNKVNLKSYNTHTLTVASS-----LRPAHPDFFVKKVVRVVDKEDNTLEM 112
QY 50 -FKESIKFIHCRLRGESCLVHCLAGVRSVTLVATYMTYTDGWMEDALHTVRAGRSCA 108
DQ 113 YFDECVDFIDAKRGGGSLVHCFVGKRSRVTIVAYILMKRHGMLTQAOLQHVKSRRPVA 172
QY 109 NPNVGFORLOEFER 123
DQ 173 SPNAGFIROLQDLEK 187

RESULT 12
Q9LUG6 PRELIMINARY; PRT: 198 AA.

AC Q9LUG6 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DUAL-SPECIFICITY PROTEIN PHOSPHATASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=2027480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones";
RL DNA Res. 7:131-135(2000).
DR EMBL: AB023036; BAB02780.1; -
DR InterPro: IPR000340; DS_phosphatase.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00782; DSPC; 1.
DR SMART: SM00195; DSPC; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE.2; 1.
DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 198 AA; 22113 MW; 815BCBE3BFB696A CRC64;

Query Match 22.9%; Score 205; DB 10; Length 198;
Best Local Similarity 37.8%; Pred. No. 8.2e-14;
Matches 51; Conservative 14; Mismatches 44; Indels 26; Gaps 2;

QY 11 GLYIGNEFKDARDADQLSKNKVTHILSVHDSFGLCWRTH----- 49
DQ 57 GLYIGSVAAASNKVNLKSYNTHTLTVASS-----LRPAHPDFFVKKVVRVVDKEDNTLEM 112
QY 50 -FKESIKFIHCRLRGESCLVHCLAGVRSVTLVATYMTYTDGWMEDALHTVRAGRSCA 108
DQ 113 YFDECVDFIDAKRGGGSLVHCFVGKRSRVTIVAYILMKRHGMLTQAOLQHVKSRRPVA 172
QY 109 NPNVGFORLOEFER 123

DQ 173 SPNAGFIROLQDLEK 187

RESULT 13
ID 013632 PRELIMINARY; PRT: 330 AA.
AC 013632;

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PROTEIN-TYROSINE PHOSPHATASE YVH1.
GN P1040 OR SPAC17A3.06.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972 H-;
RA Kushida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J.,
RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,
RA Ogura K., Otsuka R., Kudoh Y., Yanagida M., Machida M., Zhang M.Q.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Wood V., Skellon J., Churcher C.M., Rajandream M.A., Barrell B.G.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB004537; BAA21420.1; -
DR EMBL: AL109652; CAB51765.1; -
DR HSRP: Q16828; IMRP.
DR InterPro: IPR000340; DS_phosphatase.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00782; DSPC; 1.
DR SMART: SM00195; DSPC; 1.
DR SMART: SM00012; PTPC; DSPC; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE.2; 1.
DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 330 AA; 38006 MW; DBF64E7FAEBA1E84 CRC64;

Query Match 22.5%; Score 202; DB 3; Length 330;
Best Local Similarity 32.3%; Pred. No. 3.1e-13;
Matches 52; Conservative 26; Mismatches 59; Indels 24; Gaps 4;

QY 3 NGMNKILPGLYIGNEFKDARDADQLSKNKVTHILSVHD--SPGL-----CWR----- 46
DQ 45 NDLSELKRLYLSSWKRTASLSTDKGIDYLSAMSINPNLSVPEQGHLMQIDSSQ 104
QY 47 --TRFKESIKFIHCRLRGESCLVHCLAGVRSVTLVATYMTYTDGWMEDALHTVRAG 104
DQ 105 NILQYFEKSNKFIKALSKNAKVLVHCFAGISRSVTLVAYILMKRNNMTFALSHINER 164
QY 105 RSCAMPNNGFOROLOEFER-----HEVQYQWMLKEEIGE 139
DQ 165 RSGISPNANFLRLQRYFECNYOLDRLSLRPYRWMLFRRYGD 205

RESULT 14
ID 091663 PRELIMINARY; PRT: 378 AA.

AC 091663;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DUAL SPECIFICITY PROTEIN PHOSPHATASE ? (EC 3.1.3.48) (EC 3.1.3.16)
OS (MAP KINASE PHOSPHATASE XI(C).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYO;
RA MEDLINE=95319535; Pubmed=7541116;
RT Umlauer M., Marshall C.J., Mason C.S., Old R.W., Smith J.C.;
RL "Mesoderm induction in Xenopus caused by activation of MAP kinase";
CC Nature 376:58-62(1995).
CC -1- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
CC PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
CC TYROSINE + PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: LOCALISED IN THE BRANCHIAL ARCH REGION AND
CC TAIL TIP.
CC -1- INDUCTION: BY RETINOIC ACID.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC -1- SIMILARITY: CONTAINS THE CDC25 HOMOLOG DOMAINS 2 A AND B (CH2
CC DOMAINS A AND B).
DR EMBL: U43223; AAA85240.1; .
DR HSSP: Q16828; 1MKP.
DR InterPro: IPR000340; DS_phosphatase.
DR InterPro: IPR00387; Rhodanese_domain.
DR InterPro: IPR00387; TYR_phosphatase.
DR Pfam: PF00782; DSPC; 1.
DR SMART: SM00195; DSPC; 1.
DR SMART: SM00450; RHOD; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW Hydrolyase.
FT DOMAIN 34 49 CH2 B DOMAIN.
FT DOMAIN 126 141 CH2 B DOMAIN.
FT DOMAIN 152 158 POLY-SER.
FT DOMAIN 205 378 CATALYTIC.
FT ACT_SITE 290 BY SIMILARITY.
SQ SEQUENCE 378 AA; 42036 MW; F274DACA960B783 CRC64;

Query Match 22.2%; Score 199; DB 13; Length 378;
Best Local Similarity 35.9%; Pred. No. 7.7e-13;
Matches 51; Conservative 23; Mismatches 38; Indels 30; Gaps 4;

QY 7 KILPLGYIGNFKDARDAEQLSKNKVTHLSV-----HDSPL 43
DB 206 ELPLPLLYLGCAKDSYTNLLEFGIKYILNVTPNLPNLEFNAGEFRYKQIPISDHWSNL 265
QY 44 CWRTRHFKESIKFIHECRLGESG--LVHCLAGVSRYTLVAYIMTVTDGFMEDALHTV 101
DB 266 ---SQFPEAITSFIDEA--RGKSGVLVHCLAGISRYTVYAVYIMOKLNLSDNDAYDIY 320
QY 102 RAGRCANPNVGFQROLOEFK 123
DB 321 KMKKSNISPNFNMGLDPER 342

RESULT 15
099KC2
ID 099KC2 PRELIMINARY; PRT; 436 AA.
AC 099KC2:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SIMILAR TO DUAL SPECIFICITY PHOSPHATASE 9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC004738; AAH04738.1; .
SQ SEQUENCE 436 AA; 47088 MW; C4160F40DE263147 CRC64;

Query Match 22.2%; Score 199; DB 11; Length 436;
Best Local Similarity 35.0%; Pred. No. 9.1e-13;
Matches 49; Conservative 22; Mismatches 43; Indels 26; Gaps 2;

QY 7 KILPLGYIGNFKDARDAEQLSKNKVTHLSV-----HDSPL 43
DB 258 QILPNLYLSARDSANLESIAKIGIRYILNVTPNLPNLEPKNDPFHKQIPISDHWSNL 317
QY 44 CWRTRHFKESIKFIHECRLGESGVLHCLAGVSRYTLVAYIMTVTDGFMEDALHTV 103
DB 318 ---SQFPEAIAFIDEALSQNGVLVHCLAGVSRYTVYAVYIMOKLNLSDNDAYDLVKR 374
QY 104 GRGCANPNVGFQROLOEFK 123
DB 375 KRSNISPNNFNMGLDPER 394

Search completed: February 12, 2002, 16:16:27
Job time: 191 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 16:10:01 ; Search time 12.59 Seconds

(without alignments)
298.495 Million cell updates/sec

Title: US-09-544-525-2

Perfect score: 897

Sequence: 1 MGNMKNKILPGLYIGNFKDA.....AKNIIAAPGILKFWAFRLRL 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	20.7	397	2	US-08-990-379-8
2	169.5	18.9	207	4	US-09-013-881-4
3	168	18.7	353	4	US-09-013-881-3
4	167.5	18.7	226	4	US-09-045-973-8
5	161	17.9	367	2	US-08-530-290-24
6	159	17.7	393	2	US-08-990-379-4
7	159	17.7	394	2	US-08-530-290-23
8	159	17.7	395	2	US-08-990-379-5
9	158	17.6	263	4	US-09-164-193-5
10	156	17.4	313	2	US-08-990-379-7
11	156	17.4	314	2	US-09-164-193-22
12	152.5	17.0	198	4	US-09-163-833-2
13	152	16.9	367	2	US-08-990-379-6
14	150.5	16.8	198	4	US-09-045-973-5
15	147.5	16.4	185	1	US-07-988-273-2
16	147.5	16.4	185	3	US-08-848-810-25
17	147.5	16.4	185	4	US-09-164-193-21
18	147.5	16.4	185	5	PCT-US93-12019-2
19	143	15.9	72	2	US-08-530-290-20
20	138	15.4	117	1	US-07-988-273-4
21	138	15.4	117	5	PCT-US93-12019-4
22	121	13.5	72	2	US-08-530-290-19
23	109.5	12.2	116	1	US-07-988-273-5
24	109.5	12.2	116	5	PCT-US93-12019-5
25	99.5	11.1	118	1	US-07-988-273-3
26	99.5	11.1	118	5	PCT-US93-12019-3
27	99	11.0	201	2	US-08-933-750C-21

28	99	11.0	201	4	US-09-234-613-21	Sequence 21, Appl
29	91.5	10.2	150	4	US-09-164-193-23	Sequence 23, Appl
30	86	9.6	209	4	US-09-164-193-8	Sequence 8, Appl
31	77.5	8.6	173	3	US-08-725-532A-3	Sequence 3, Appl
32	77	8.6	2465	2	US-08-596-291-3	Sequence 3, Appl
33	77	8.6	2465	3	US-09-100-804-3	Sequence 3, Appl
34	77	8.6	2466	3	US-09-080-855-12	Sequence 12, Appl
35	77	8.6	2466	5	PCT-US94-09943-2	Sequence 2, Appl
36	77	8.6	2485	4	US-09-230-640-46	Sequence 46, Appl
37	75.5	8.4	173	4	US-09-164-193-2	Sequence 2, Appl
38	75	8.4	212	1	US-08-461-859-35	Sequence 35, Appl
39	74	8.2	231	2	US-08-446-345-37	Sequence 37, Appl
40	74	8.2	242	2	US-08-685-992-21	Sequence 21, Appl
41	74	8.2	242	2	US-09-144-925-21	Sequence 21, Appl
42	73	8.1	45	2	US-08-530-290-21	Sequence 2, Appl
43	73	8.1	820	1	US-08-166-717D-6	Sequence 6, Appl
44	72	8.0	299	2	US-08-701-191A-13	Sequence 13, Appl
45	72	8.0	300	2	US-08-701-191A-31	Sequence 31, Appl

ALIGNMENTS

```
RESULT 1
US-08-990-379-8
: Sequence 8, Application US/08990379
: Patent No. 5998188
:
: GENERAL INFORMATION:
: APPLICANT: Stork, Philip J
: TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
: TITLE OF INVENTION: Their Biologically Active Expression Products
: FILE REFERENCE: 4104-000322USA
: CURRENT APPLICATION NUMBER: US/08/990.379
: CURRENT FILING DATE: 1997-12-15
: EARLIER APPLICATION NUMBER: PCT/US96/10402
: EARLIER FILING DATE: 1996-06-14
: EARLIER APPLICATION NUMBER: 60/000.263
: EARLIER FILING DATE: 1995-06-16
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 397
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-990-379-8

Query Match 20.7%; Score 186; DB 2; Length 397;
Best Local Similarity 33.6%; Pred. No. 1.5e-14;
Matches 46; Conservative 21; Mismatches 52; Indels 18; Gaps 1;

QY 4 GNNKILPGLYIGNFKDAEQLSRNKYTHILSDPGLCWTR----- 48
DB 177 GVEILPFLYLSAHHASCEFLANLHTALLNVSRRSEACMTHHYKWIIVEDSHTD 236
QY 49 ---HRESKIFTEHRCLESCVLCAGVSSVTLVAVINTVDFGMDALHTVRAGR 105
DB 237 ISSHFOEALDFIDCKREKGVLCVHCAGISSRPTICMAYLMKTRQFRLEAFDYIKRR 296
QY 106 SCANNVGFQROLOFE 122
DB 297 SWVSPNFGFMGLDYE 313

RESULT 2
US-09-013-881-4
: Sequence 4, Application US/09013881
: Patent No. 6132964
:
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Lal, Preeti
: APPLICANT: Hillman, Jennifer L.
```

```
Query Match      18.9% ; Score 169.5; DB 4; Length 207;
Best Local Similarity    31.0%; Pred. No. 6.4e-13;
Matches 46; Conservative   24; Mismatches 52; Indels   31; Gaps     5;

QY          3 NGNMKILPGLYIGNFKDARDAEOLSKNVTHILLSVHDSFGLCWR----- 46
              |::|::||::|: : ::|::|: ||
Db           60 NHADEWVGTLGDDMMANNRRRLRDLITVHLANSHR---WRGTPEAYEGSLIRYLGV 116
              |::|::||::|: : ::|::|: ||

QY          47 -----TRHEESIKFTHECRLR-GESCLVNCACVSSTVLVIATMTVDCEMEDALH 99
              |::|: ||::| 111 |111 |111 |111 |:|:|
Db           117 EPAFDMSIHFFOTADFIHALSOPGGKLTVHCAGSVSRATLVLYLMLIHNHTLLVEAIK 176
              |::|: ||::| 111 |111 |111 |111 |:|:|

QY          100 TVRAGSCAPANGVFOROLEEFKEHVHQYOHWMLK 134
              |:| |111|111|::|:|:|:|
Db           177 KYKDHRGIT-PNRGFLROLLALDR----RLRGGLE 206

RESULT       3
US-09-013-881-3
Sequence 3, Application US/09013881
Patent No. 6133964

GENERAL INFORMATION:
APPPLICANT: Bandman, Olga
APPPLICANT: Lal, Preetl
APPPLICANT: Hillman, Jennifer L.
APPPLICANT: Corley, Neil C.
APPPLICANT: Guessler, Karl J.
APPPLICANT: Shah, Purvi

TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
```

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Query Match Summary: 18.7% Score 168; DB 4; Length 353;
Best local similarity 29.3%; Pred. No. 2.1e-12;
Matches 49; Conservative 27; Mismatches 59; Indels 32; Gaps 6.

QY      5 MNKLTIGLYIGNEFKDARBAEQLSKNKVTHIISVD-----SFGI--CWR-----46
Db      40 MEVQGPGLYFGCAAAVAEPDHLREAGITAVLTVDSSEPSFKAGGVEDMLRLEVPALDLP 99
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      47 ----THRESIKETHECRIGRESGLVCLAGVSRSYTLVATIMYTTDGMEDALHYR 102
Db      100 EFDLISHDRCAFLFGQAABEGRAVLVCHGAGVSVAIIITAFILMKTDLPFEKAYEKQL 159
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      103 AGRSKANNVGFQROLOEFER--HEV-----HQYR-OMLKEEGE 139
Db      160 ILKPEAKNKEGFEMQLKLYQAMGEVDISSAIYQYVRLQKVTERTYPE 206
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
US-09-045-973-8
; Sequence 8, Application US/09045973
; Patent No. 6165767
;
GENERAL INFORMATION:
APPLICANT: tal, preeti
APPLICANT: yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: PROTEIN PHOSPHATASE RELATED MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

```

STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,973
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0491 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1495338
US-09-045-973-8

Query Match 18.7%; Score 167.5; DB 4; Length 226;
Best Local Similarity 28.6%; Pred. No. 1.3e-12;
Matches 48; Conservative 33; Mismatches 58; Indels 29; Gaps 5;
QY 5 MNKILPGIYGNFKARAEQLSKNKYTHILSV-----SPGLCKRTR----- 48
DB 14 MSEIPLGFLICGV-SALSKEDEKKRKHITHIINATTEVPNLRSLGIQFTKMLIEDTPQY 72
QY 49 ---HKESIKFHECRLEGESCLVAGSRSVTLVATYMTVDFGMDALHTVRAGR 105
DB 73 IYPLELSDQIOLIALDAGKYLHCVAGVSRSASICLAFILKTYCRMLREYVHLMKSR 132
QY 106 SCANPNVGFQROLOEFKEHEVHQYRWMLKEEGESPL-QDAEEAKNII 152
DB 133 SMVRNGLGFWRLIAYEON-----VKENAGSVRLVRDEAQPOLL 172

RESULT 5
US-08-530-290-24
Sequence 24, Application US/08530290
Patent No. 5958721
GENERAL INFORMATION:
APPLICANT: Marshall, Christopher John
APPLICANT: Ashworth, Alan
APPLICANT: Hughes, David Anthony
TITLE OF INVENTION: Methods for Screening of Substances for
TITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,290
FILING DATE: 14-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/00694
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9402573.1
FILING DATE: 10-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9307250.2
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 084611-00000005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-530-290-24

Query Match 17.9%; Score 161; DB 2; Length 367;
Best Local Similarity 29.8%; Pred. No. 1.6e-11;
Matches 42; Conservative 20; Mismatches 53; Indels 26; Gaps 2;
QY 4 GNMKILPGIYGNFKARAEQLSKNKYTHILSV-----HDSPL 41
DB 173 GVEILPLFLYGSAYHASKMDLALGITALLINVSANCPNHFEGHYQKSIPEVDNHRAD 232
QY 42 GICMTRHFKESIKFHECRLEGESCLVAGSRSVTLVATYMTVDFGMDALHTV 101
DB 233 ISSW----FNEAIDFIDISIKNAGRGVFWCQGISRSATICLAYIMRTNRVXLDEAFERY 288
QY 102 RAGRCANPNVGFQROLOEFE 122
DB 289 KORSLISPNFSEWGLLOFE 309

RESULT 6
US-08-990-379-4
Sequence 4, Application US/08990379
Patent No. 5998188
GENERAL INFORMATION:
APPLICANT: Stock, Phillip J
APPLICANT: Mista-Press, Anita
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
TITLE OF INVENTION: Their Biologically Active Expression Products
FILE REFERENCE: 4104-000320USA
CURRENT APPLICATION NUMBER: US/08/990,379
EARLIER FILING DATE: 1997-12-15
EARLIER APPLICATION NUMBER: PCT/US96/10402
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: 60/000,263
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 393
TYPE: PRT
ORGANISM: Rattus norvegicus
US-08-990-379-4

Page 4

[illegible]

EARLIER APPLICATION NUMBER: PCT/US96/10402
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: 60/000,263
EARLIER FILING DATE: 1995-06-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO: 6
LENGTH: 367
TYPE: PRT
ORGANISM: Mus sp.
US-08-990-379-6

Query Match 16.9%; Score 152; DB 2; Length 367;
Best Local Similarity 29.1%; Pred. No. 2.1e-10;
Matches 41; Conservative 20; Mismatches 54; Indels 26; Gaps 2;

QY 4 GNMKILPGIYICNFKDAEQLSKNKVTHILSV-----HDSF 41
DB 173 GPEVILISFLIGSAYHSRDMDLALGITALINVSANCPNHFGHYQYKSIPEVDHKKAD 232
QY 42 GLCWRTHFESIKFHECRLEGSCLYHCLAGVSRYLYAYMTVDFGMDALHTYRGR 101
DB 233 ISSM-----FNEAIDFIDISIDAGRVFVHCAGISRSATICTAYIMTRNKVKIDEAFEFY 288
QY 102 RAGSCANPNVGFQROLOEPE 122
DB 289 KORRSIIPNFSEFMGQLOPE 309

RESULT 14
US-09-045-973-5
Sequence 5, Application US/09045973
Patent No. 6165767
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Tue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guebler, Karl J.
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: PROTEIN PHOSPHATASE RELATED MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,973
FILING DATE: Filed Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0491 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT16
CLONE: 3041794
US-09-045-973-5

Query Match 16.8%; Score 150.5; DB 4; Length 198;
Best Local Similarity 27.7%; Pred. No. 1.3e-10;
Matches 48; Conservative 30; Mismatches 76; Indels 19; Gaps 3;

QY 4 GNMKILPGIYICNFKDAEQLSKNKVTHILSVH-DSFGICWRT----- 47
DB 26 GIAQITSSFLIGSAYHSRDLQARGITCIYVATTEIPNFMPQFEYKVPYLDMPHAP 85
QY 48 --RHFKESIKFHECRLEGSCLYHCLAGVSRYLYAYMTVDFGMDALHTYRGR 105
DB 86 IGLYFTVADKTHSVSRKIGATLVHCAGVSRSATICTAYIMKFNHVCILLEYMVKARR 145
QY 106 SCANPNVGFQROLOEPEKHEVHQR-OWLKEEYGESEPLQDAEAKNIIAARPI 157
DB 146 PYIRPNVGFWRQIDYEROLFEGKSTVKVWQPPYGLVPPVYEKSHLMPYNGI 198

RESULT 15
US-07-988-273-2
Sequence 2, Application US/07988273
Patent No. 5512434
GENERAL INFORMATION:
APPLICANT: AARONSON, Stuart A.
APPLICANT: BOTTARO, Donald P.
APPLICANT: ISHIBASHI, Toshio
APPLICANT: MIKI, Toru
TITLE OF INVENTION: EXPRESSION CLONING OF A HUMAN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,273
FILING DATE: 19921214
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/182 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-988-273-2

Query Match 16.4%; Score 147.5; DB 1; Length 185;
Best Local Similarity 29.8%; Pred. No. 2.8e-10;
Matches 42; Conservative 20; Mismatches 50; Indels 29; Gaps 4;

BASE COUNT 233 a 230 c 242 g 221 t
 ORIGIN

Query Match 91.7%; Score 802.4; DB 6; Length 926;
 Best Local Similarity 94.4%; Pred. No. 1.4e-200;
 Matches 874; Conservative 0; Mismatches 1; Indels 51; Gaps 2;

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OY 1 cccgcgcgcctccctccctgtaacatgcatgctgctgagccacacgcgcgcgcgc 60
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OY 61 gctagcgtctgccttcacacacacatgggaatggaatgaacacacacacacacacac 120
Db 61 gctagcgtctgccttcacacacacatgggaatggaatgaacacacacacacacacac 120
OY 121 acatggcgaacttcaaatgacagagacgcgcgaacatggaacgaacgaacgctgacac 180
Db 121 acatggcgaacttcaaatgacagagacgcgcgaacatggaacgaacgaacgctgacac 180
OY 181 atattctgtctgccaagataat-ccaggcctatgttggag----- 220
Db 181 atattctgtctgccaagataat-ccaggcctatgttggag----- 220
OY 221 -----gacaagacattccaagaagaatattaat 249
Db 241 TCCACAGACGGAGATTTCACATCTCAAAACCTGACAAAGACATTTCAAAGAAAGTATTAAAT 300
OY 250 tcaattacagagtgccgcgttcgcgcgtgagagctgcctgtacacgtcgcgcgcgcgc 309
Db 301 TCATTACAGAGTCCGCGCTCCGCGGTGAGAGTCCCTTGACACTCCCTGCGCGGCTCT 360
OY 310 ccaagagcgtgacacgtgcatgcatatcatatgacacacacacacacacacacacacac 369
Db 361 CCAAGAGCGGTGACACTGCTGATGCAATCTGACCTGACACTGCTGCTGCTGCTGCTG 420
OY 370 atgcctctgcaacacgtgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 429
Db 421 ATGCTCTGACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
OY 430 gacagctcagaggtttggaagacatgagatcctatcagatcagcagtgctggaagaag 489
Db 481 GACAGCTCCAGGAGTGTGGAAGCAATGAGTCCATCATGATGCGGAGTGGCTGAAGAAG 540
OY 490 aatatgagagagcccttcgcagatgacagagacacacacacacacacacacacacacac 549
Db 541 AATATGAGAGAGCCCTTTGCAAGATGCAAGAAAGCCAAACATTTCTGGCCGCTCCAG 600
OY 550 gaattctgaagttctgagccttctcgaagaactglaattgactggaagttctgaata 609
Db 601 GAATTCGTGAAGTCTGGGCTTTCTCAGAACTGTAATGTACGTGAAGTTCTGAATA 660
OY 610 ttgcaaacccgcagaggtttgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 669
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OY 670 tatccagtagtgaattgttaaacctgttttcaattgaaagcctaatactgaaagttctg 729
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OY 730 ttaattgtagagaaactaagagatactcttaagaagaagaataatttccctatccacac 789
Db 781 TTTATGTTGAGAACTTAAGATATCTTTAGCAAGAGAAATAATTTTCCCTTATCCACAC 840
OY 790 tgcctgtagagttctgtacacgtctgtagcctgtagaagatcccggaagccttgccgc 849
Db 841 TGCTGTGAGAGTTTCTGTAACCTCGCTTGAGATCGCTGTAAGATCCCGGAGCCTTGCCGC 900
OY 850 actgcctgtggtgagcttgagcgtc 875
Db 901 ACTGCTGTGAGGTGCTTGCGGCTC 926

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RESULT 2

AX068328

LOCUS

AX068328

DEFINITION

AX068328

ACCESSION

AX068328

VERSION

AX068328.1

KEYWORDS

GI:12578509

SOURCE

human.

ORGANISM

human sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 926)

AUTHORS

Luche, R.M. and Wei, B.

TITLE

DSP-3 dual-specificity phosphatase

JOURNAL

Patent: WO 0102582-A 11-JAN-2001;

Ceplyr, Inc. (US)

FEATURES

Location/Qualifiers

1..926

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 233 a 230 c 242 g 221 t

ORIGIN

Query Match 91.7%; Score 802.4; DB 6; Length 926;

Best Local Similarity 94.4%; Pred. No. 1.4e-200;

Matches 874; Conservative 0; Mismatches 1; Indels 51; Gaps 2;

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OY 1 cccgcgcgcctccctccctgtaacatgcatgctgctgagccacacgcgcgcgcgc 60
Db 1 cccgcgcgcctccctccctccctgtaacatgcatgctgctgagccacacgcgcgcgcgc 60
OY 61 gctagcgtctgccttcacacacacatgggaatggaatgaacacacacacacacacac 120
Db 61 gctagcgtctgccttcacacacacatgggaatggaatgaacacacacacacacacac 120
OY 121 acatggcgaacttcaaatgacagagacgcgcgaacatggaacgaacgaacgctgacac 180
Db 121 acatggcgaacttcaaatgacagagacgcgcgaacatggaacgaacgaacgctgacac 180
OY 181 atattctgtctgccaagataat-ccaggcctatgttggag----- 220
Db 181 atattctgtctgccaagataat-ccaggcctatgttggag----- 220
OY 221 -----gacaagacattccaagaagaatattaat 249
Db 241 TCCACAGACGGAGATTTCACATCTCAAAACCTGACAAAGACATTTCAAAGAAAGTATTAAAT 300
OY 250 tcaattacagagtgccgcgttcgcgcgtgagagctgcctgtacacgtcgcgcgcgcgcgc 309
Db 301 TCATTACAGAGTCCGCGCTCCGCGGTGAGAGTCCCTTGACACTCCCTGCGCGGCTCT 360
OY 310 ccaagagcgtgacacgtgcatgcatatcatatgacacacacacacacacacacacacac 369
Db 361 CCAAGAGCGGTGACACTGCTGATGCAATCTGACCTGACACTGCTGCTGCTGCTGCTG 420
OY 370 atgcctctgcaacacgtgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 429
Db 421 ATGCTCTGACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
OY 430 gacagctcagaggtttggaagacatgagatcctatcagatcagcagtgctggaagaag 489
Db 481 GACAGCTCCAGGAGTTTGAAGATGATGCTGCAAGAGTCCATCATGATGCGGAGTGGCTGAAGAAG 540
OY 490 aatatgagagagcccttcgcagatgacagagacacacacacacacacacacacacacac 549
Db 541 AATATGAGAGAGCCCTTTGCAAGATGCAAGAAAGCCAAACATTTCTGGCCGCTCCAG 600
OY 550 gaattctgaagttctgagccttctcgaagaactglaattgactggaagttctgaaata 609
Db 601 GAATTCGTGAAGTCTGGGCTTTCTCAGAACTGTAATGTACGTGAAGTTCTGAATA 660
OY 610 ttgcaaacccgcagaggtttgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 669

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OY 730 ttatgtgtggaactaagatattctttagcaagaagaataatttcccttatacccaac 789
Db 781 TTTATGTTGAGAACTAAGATATTCTTTAGCAAGAGAAATATTTCCTTATCCCCAC 840
OY 790 tgcgtggaagtttcttactcgttgatgctgtgaagatccggaggacgttgcgcg 849
Db 841 TGCGTGAGAGTTCTTACTCGCTTGAGATGCTGTGAAGATCCGGAGCCTTGCCGC 900
OY 850 actgcctgtggtgtgcttgagctc 875
Db 901 ACTGCCCTTGAGGTGGCTTGCGCTC 926

RESULT 3
AX086014 AX086014 1379 bp DNA PAT 09-MAR-2001
LOCUS Sequence 11 from Patent WO0112819.
DEFINITION AX086014
ACCESSION AX086014
VERSION AX086014.1 GI:13275838
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1379)
Ploman, G.D., Martinez, R., Whyte, D., Hill, R., Flanagan, P. and
Joubin, M.
TITLE Protein phosphatases and diagnosis and treatment of
phosphatase-related disorders
JOURNAL Patent: WO 0112819-A 11 22-FEB-2001;
Sugen, Inc. (US)
FEATURES
Location/Qualifiers
source 1..1379
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 298 a 374 c 386 g 320 t 1 others
ORIGIN
Query Match 91.3%; Score 799.2; DB 6; Length 1379;
Best Local Similarity 94.2%; Pred. No. 1e-199;
Matches 872; Conservative 0; Mismatches 3; Indels 51; Gaps 2;

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OY 370 atgcccgcgaacacgtgtgtccgggaagatcctgtgcaaccccaagctgggtccaga 429
Db 677 ATGCCCTGACACCCGTGCTGCTGGAGATCTCTGTGCCAACCCACAGCTGGGCTCCAGA 736
OY 430 gacagctccaaagatttgagaagcatgagtcacatcagatcagtcagtgctgaagaag 489
Db 737 GACAGCTCCAGAGATTGAGAAAGCATAGAGTCCATCATATCGGACATGGGTGAAGAAG 796
OY 490 aatctggagaagcccttgcagagatgcagaagaagccaaacaacatttgcgcgtccag 549
Db 797 AATATGAGAGAGCCCTTTCAGAGATGCAGAAAGCCAAAACATTCCTGGCCGCTCCGG 856
OY 550 gaattctgaagttctgggaccttctcagaagaacgtatgtactcgaagtttctgaata 609
Db 857 GAATTCGTGAAGTTCTGGGCTTCTTCAGAAACGTGTATGTAACCTGAAGTTTCTGAATA 916
OY 610 ttgcaaacccgacagatttagcgtgtgtgtccaaagaagaagaacacatagatttaag 669
Db 917 TTGCAAAACCCACAGATTAGGCTGTGCTGCCAAAAGAAAAGCAACATAGATTTAAG 976
OY 670 laticagtagtattgtaactgttttcaatttgaagcgaalatalacgtatcatg 729
Db 977 TATCAGTAGTAGATTGTAAGCTGTTTTCATTGTAAGCTGATATATAGTAGTCATG 1036
OY 730 ttatgtgtggaactaagatattctttagcaagaagaataatttcccttatacccaac 789
Db 1037 TTTATGTTGAGAACTAAGATATTCTTTAGCAAGAGAAATATTTCCTTATCCCCAC 1096
OY 790 tgcgtggaagtttcttactcgttgatgctgtgaagatccggaggacgttgcgcg 849
Db 1097 TGCGTGAGAGTTCTTACTCGCTTGAGATGCTGTGAAGATCCGGAGCCTTGCCGC 1156
OY 850 actgcctgtggtgtgcttgagctc 875
Db 1157 ACTGCCCTTGAGGTGGCTTGCGCTC 1182

RESULT 4
AF165519 AF165519 1092 bp mRNA PRI 20-JUL-2000
LOCUS AF165519
DEFINITION human sapiens mitogen-activated protein kinase phosphatase x (MKPX)
ACCESSION AF165519
VERSION AF165519.1 GI:9294744
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1092)
TITLE Gu, J., Huang, Q., Yu, Y., Xu, S., Wang, Y., Han, Z., Zhou, J.,
AUTHORS Tu, Y., Gu, W., Fu, G. and Huang, C.
Novel genes expressed in hematopoietic stem/progenitor cells from
Myelodysplastic Syndromes patient
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1092)
AUTHORS Gu, J., Huang, Q., Yu, Y., Xu, S., Wang, Y., Han, Z. and Chen, Z.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1999) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, P. R. China
FEATURES
Location/Qualifiers
source 1..1092
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="hematopoietic stem/progenitor cell"
1..1092
/gene="MKPX"

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Db	609	TTTCGAATATTGCNA-----AGTTCAGGCTGGTCTCCAAAAAGAAAGTGAAGT	660
Qy	660	agag-----ttaagatccagtagtgatcttgtaaacctg---ttttcatctgaagc	709
Db	661	AAATTTATTTTAAAGATCCAAATAGCATTTGTATATCTTTTATTTTCAATTTTAAC	720
Qy	710	tgaataatacgtagtcagtcgtt----tatgttgaagactaagatatctttagaagag	765
Db	721	CAATGCATGTATATCATCTGTTGGAATATGTTAAGATGTATAGCATTTCTGTAGCANAAG	780
Qy	766	aaaatatttcccccttatccccaactgcgtgtagagttctc	805
Db	781	AAAAATATCTTGCCCTTAACTCCATCGCTGAGTGTTGTTCTT	820

RESULT	6				
LOCUS	AF237619				
DEFINITION					
ACCESSION	AF237619	1067 bp	mRNA	17-JUL-2001	
VERSION	AF237619				
KEYWORDS	AF237619.1	GI:13183068			
SOURCE					
ORGANISM	house mouse.				
	Mus musculus				
REFERENCE					
AUTHORS	Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu				
TITLE	1 (bases 1 to 1067)				
	Aoyama, K., Nagata, M., Oshima, K., Matsuda, T. and Aoki, N.				
JOURNAL	Molecular cloning and characterization of a novel dual specificity				
MEDLINE	phosphatase, Lmw-DSP2, that lacks the Cdc25 homology domain				
PUBMED	J. Biol. Chem. 276 (29), 27575-27583 (2001)				
REFERENCE	21347909				
AUTHORS	11346645				
TITLE	2 (bases 1 to 1067)				
JOURNAL	Aoyama, K., Matsuda, T. and Aoki, N.				
	Direct Submission				
	Submitted (19-FEB-2000) Applied Molecular Biosciences, Nagoya				
	University, Furo-cho, Chikusa-ku, Nagoya, Aichi 464-8601, Japan				
	Location/Qualifiers				
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FEATURES					
source	/organism="Mus musculus"				
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CDS	28. .562				

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DAEAKRIILAPGLIKTWAFRLR"
BASE COUNT      301 a      223 c      260 g      283 t
ORIGIN

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	Best Local Similarity	79.8%	Pred. No. 3.6e-107		
	Matches 633	Conservative 0	Mismatches 187	Indels 73	Gaps
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Db	22	gcggccatggggagagggatgagccacagatcctgcggcgccctgtacattggcgaacttcaaa	81		
QY	138	gatgcacaagagcggcggaacaattggcgaaagaaagcggcaacatattcgtcttccac	197		
Db	82	gacgcacaaagatgacgaacacgtttggcaggaacaaggatgacacacattcttcttctggc	141		

QY	198	gaaagtc-ccagagcctatgttggag-----	220
Db	142	GATACtGtCCAGGcCCcATGtTtGGAGGcAGtTAAATtACCTGtGTtTCCAGGcGAGAcACA	201
QY	221	-----gacaagacatttcaaagaagaagtataaattcaattcaacgagtgccgg	266
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QY	267	ctccgcgvgagagcgtgcttgtacacctgcgcggcggggtctcagagcgttgacactg	326
Db	262	CTCCAGGGGTGAGAGcCTGtCTTGTATCAATtTGcCTGGcTGGGGGTCTCCAGAGATGtGACATtG	321
QY	327	gtgatgcatacaatcatgtaccgcgtcactgcacttggctcgtggagagatgcccgcacaccggt	386
Db	322	GTGATCCCAATACATCAAGACTGTACACGACTTtGGcTGGGAAATcCTTtGCACACTGtT	381
QY	387	cgctccggagatctcgtgtgcaaccccaacgctggccttccaagagacgtccagagatt	446
Db	382	CGtCGGGGGAGtGCTGTGTGCCAACCCCAcCTGGcCTTtCAAAAGCAcGTGCAGAGtTT	441
QY	447	gagaagaatgaagttccalcagtlacggtggcgttgaaggagaatataggaagagccct	506
Db	442	GAGAAcATGAAGtGtGACCCAGTATGGGCATtGGcTtGAGAAAGATGAGAGAAcCCT	501
QY	507	ttgcagagatgcagaagaagacccaaaacatctcgtgcgtccacaggaattctgaagttcgg	566
Db	502	TTGGGGGATTCAGAGAAcGCAAAATAATtCTGGcTCCcCCGGGAATtCTGAGATtACTGg	561
QY	567	gccccttctagaagacgtgtaatgtlactgtgaagtttctggaatatltgcaaccgcgagagt	626
Db	562	GcCTTTCTCGAAGAcGTATGATGTACCTGAAGTtTGAAATtTTCOA-----AGT	613
QY	627	ttagcgtggtgcctccaaaagaagaagaacacatagag-----ttaagrtacagtagt	680
Db	614	TCAAGcTGGtGCTtCCAAAAAGAAAGATGATGAACtTtATTTTtTAAGATtCCATAGt	673
QY	681	gatttgtaaacttg-----tttctcaatttgaagcttgaatatatacgtatgaatgt-----t	732
Db	674	GATTGTATtACTGTtTTTTTTTCATtTtTAACCAATtGCATGAATATCATtTTTGGAAAT	733
QY	733	atgtltggaacaaagatatctttagcaagagaanaatatlttcccctatcccacatgc	792
Db	734	ATGTGAAGATCTATGATtATtCTGTAGCAAGAGAAATATCTTtGcCTTtAACTCCACtGC	793
QY	793	tgttgaggttctc 805	
Db	794	TGTGtGTGTCT 806	

RESULT	7
AX068352	
LOCUS	
DEFINITION	AX068352 555 bp DNA
ACCESSION	Sequence 25 from Patent WO0102582.
VERSION	AX068352
KEYWORDS	AX068352.1 GI:12578520
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 555)
AUTHORS	Inche,R.M. and Wei,B.
JOURNAL	Dsp-3 dual-specificity phosphatase Patent: WO 0102582-A 25 11-JAN-2001;
FEATURES	Ceptyr, Inc. (US) Location/Qualifiers 1..555 /organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	149 a 136 c 154 g 116 t
ORIGIN	

Query Match 49.3%; Score 431.4; DB 6; Length 555;
 Best Local Similarity 90.6%; Pred. No. 7.4e-103;
 Matches 503; Conservative 0; Mismatches 1; Indels 51; Gaps 2;

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OY 84 atggggaatggatgaacaagatcctgcggcgctgtacatcggcgaactcaaatgtgc 143
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OY 144 agagaagcggaacatctggcaagaacaggtgacacatctgtctgtccacgtagt 203
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DB 61 AGAGAGCGCGAACAATTGAGCAAGAACAGAGTACATATTCTGTCTCCACGATAGT 120
OY 204 -ccagagcctatgttgag- 220
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DB 121 GCCAGGCTATGTTGGAGGAGATTAAATACGTGTGATCCAGACGGGATTCAACATCT 180
OY 221 -gacaagaattccaagaagaatataatcattcacaagatgcccgtccgc 272
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DB 181 CAAACCTGACAAAGACATTTCAAGAAATATTAAATTATTCACAGTCCGCGCTCCG 240
OY 273 ggtgagaagctgctgtacacatgcctgcggcggtctccagagacgtgacactgtgac 332
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DB 241 GGTGAGAGTGCCTTGTACACTGCTGCGCGGGGTCTCCAGAGCGTGCACACTGGTGATC 300
OY 333 gcatcacatcatgaccgtcactgacttggcttgaggagatgcctgcacacgltgcgtcc 392
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DB 301 GCATCATCATGATGACCGTGCACGCTTGGCTGGAGAGATGCCCTGCACACGCTGCT 360
OY 393 gggagaatcctgtgccaaccccaagctgggtctccagagacagctccaggagttgagaag 452
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DB 361 GGGAGATCTCTGTGCCAACCCCAAGCGGCTTCCAGAGACACTCCAGAGATTGGAAG 420
OY 453 catgagtcacatcatgctgagctgagctgagaagaatgatgagaagcccttggcag 512
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DB 421 CATGAGTCCATCATGATGCGCATGCTGGAAGAAATATGAGAGGCGCTTGGCAG 480
OY 513 gatgagaagaagccaacaacatctgcgcgtccaggaattcgaagttcgtgcctt 572
    |||||||
DB 481 GATGAGAGAAAGAACAAAACATCTGGCGCTCCAGGAATTCTGAGTTCTGGGCTTT 540
OY 573 ctcagaagaagcttaa 587
    |||||||
DB 541 CTCAGAGAGCTGTAA 555
  
```

RESULT 8
 LOCUS AL365272 132449 bp DNA PRI 23-DEC-2000
 DEFINITION Human DNA sequence from clone RP11-328C17 on chromosome 6, complete
 sequence.
 ACCESSION AL365272
 VERSION AL365272.20 GI:11991402
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 132449)
 AUTHORS Heath, P.
 TITLE Direct Submission
 JOURNAL Submitted (23-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 On Dec 24, 2000 this sequence version replaced gi:11875910.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known

annotated repeat sequence elements. Where the sequence is
 ambiguous, there is an annotation using the 'unsure' feature key.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
 on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone configs of human
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
 Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6>
 RP11-328C17 is from the library RP11-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-328C17 it may be shorter because we sequence overlapping
 sections only once, except for a 100 base overlap.
 The true right end of clone RP11-328C17 is at 132449 in this
 sequence. The true left end of clone RP11-233K4 is at 64893 in this
 sequence. The true right end of clone RP3-416J7 is at 100 in this
 sequence. The true right end of clone RP1-125A24 is at 61243 in
 this sequence.

FEATURES

source
 Location/Qualifiers
 1..132449
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="RP11-328C17"
 /clone_11b="RP11-11.2"
 1..1562
 /note="LIM4 repeat: matches 4133..5719 of consensus"
 1563..1641
 /note="MLT1A2 repeat: matches 1..80 of consensus"
 1649..2199
 /note="LIM4 repeat: matches 3396..3937 of consensus"
 2200..2474
 /note="AluX repeat: matches 38..312 of consensus"
 2475..4279
 /note="LIM4 repeat: matches 1666..3396 of consensus"
 4306..4589
 /note="LIM4 repeat: matches 1254..1544 of consensus"
 complement(4704..5324)
 /note="match: GSS: Em:AQ628183"
 4799..4938
 /note="LIM4 repeat: matches 785..924 of consensus"
 complement(4809..5326)
 /note="match: GSS: Em:AQ774852"
 complement(4860..5272)
 /note="match: GSS: Em:AQ787689"
 4943..5094
 /note="LIM4 repeat: matches 272..420 of consensus"
 complement(5020..5329)
 /note="match: GSS: Em:AQ494601"
 5142..5435
 /note="MLT1D repeat: matches 170..428 of consensus"
 5436..5744
 /note="AluX repeat: matches 1..310 of consensus"
 5745..5869
 /note="MLT1D repeat: matches 428..568 of consensus"
 6450..6686
 /note="MIR repeat: matches 7..261 of consensus"
 6916..7994
 /note="LIM4 repeat: matches 3582..4688 of consensus"
 7984..8050
 /note="LIMB8 repeat: matches 5808..5884 of consensus"
 8064..8169
 /note="LIM4 repeat: matches 3479..3593 of consensus"
 8178..8224
 /note="LIMB4 repeat: matches 6124..6169 of consensus"
 8225..8525
 /note="AluX repeat: matches 1..301 of consensus"
 8526..8915

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misc_feature /note="LIMB4 repeat: matches 5725. .6124 of consensus"
complement(8862. .9353)
repeat_region /note="match: GSS: Em:AQ355497"
9029. .9150
/note="2 copies 61 mer 95% conserved"
misc_feature complement(9052. .9484)
/note="match: GSS: Em:AQ175845"
9388. 9675
/note="match: GSS: Em:AQ135206"
misc_feature 9487. .9840
/note="match: GSS: Em:AQ171684"
misc_feature 9491. .9932
/note="match: GSS: Em:AQ147759"
repeat_region 9524. .9697
/note="MER33 repeat: matches 1. .189 of consensus"
10046. .10143
/note="2 copies 49 mer 91% conserved"
repeat_region 11168. .11361
/note="MUT1B repeat: matches 101. .309 of consensus"
11448. .11756
/note="AluY repeat: matches 1. .309 of consensus"
repeat_region 12109. .12515
/note="L2 repeat: matches 1747. .2155 of consensus"
12798. .12947
/note="MIR repeat: matches 29. .206 of consensus"
12975. .13026
/note="MIR repeat: matches 186. .237 of consensus"
13005. .13103
/note="L2 repeat: matches 2417. .2516 of consensus"
13331. .13664
/note="MUT1B repeat: matches 4. .361 of consensus"
13704. .13907
/note="L2 repeat: matches 297. .511 of consensus"
1450. .15530
/note="L2 repeat: matches 2668. .2749 of consensus"
15876. .15935
/note="2 copies 30 mer 100% conserved"
repeat_region 16202. .16294
/note="MER81 repeat: matches 2. .94 of consensus"
17335. .17668
/note="match: GSS: Em:AQ104665"
17419. .17715
/note="AluX repeat: matches 1. .296 of consensus"
17995. .18362
/note="match: GSS: Em:AQ151578"
repeat_region 19374. .19496
/note="L2 repeat: matches 2579. .2709 of consensus"
20271. .20430
/note="MER20 repeat: matches 55. .218 of consensus"
21095. .21389
/note="AluX repeat: matches 1. .295 of consensus"
21830. .21946
/note="MIR repeat: matches 42. .152 of consensus"
22328. .22772
/note="L2 repeat: matches 2242. .2710 of consensus"
22768. .22848
/note="L2 repeat: matches 2661. .2750 of consensus"
23314. .24204
/note="CpG island"
misc_feature /evidence=not_experimental
23596. .23601
/note="Weak data."
repeat_region 23664. .25783
/note="L2 repeat: matches 2588. .2741 of consensus"
25786. .26131
/note="MER33 repeat: matches 1. .324 of consensus"
26858. .27183
/note="AluY repeat: matches 1. .301 of consensus"
27208. .27334
/note="MIR repeat: matches 81. .221 of consensus"
27673. .27833
/note="MIR repeat: matches 7. .175 of consensus"
misc_feature complement(28112. .28516)

misc_feature /note="match: GSS: Em:AQ212338"
28535. .29088
/note="match: GSS: Em:B51862"
repeat_region 28560. .28684
/note="MIR repeat: matches 79. .210 of consensus"
28588. .28828
/note="match: GSS: Em:B78941"
misc_feature 28588. .28841
/note="match: GSS: Em:B88272"
repeat_region 28849. .29048
/note="MER20 repeat: matches 2. .214 of consensus"
30148. .30232
/note="L2 repeat: matches 2610. .2692 of consensus"
misc_feature complement(31265. .31662)
/note="match: GSS: Em:AQ625926"
misc_feature complement(31333. .31662)
/note="match: GSS: Em:AQ625934"
misc_feature complement(31491. .31857)
/note="match: GSS: Em:AQ131221"
repeat_region 31733. .31875
/note="L2 repeat: matches 2039. .2197 of consensus"
repeat_region 33899. .33992
/note="L2 repeat: matches 2578. .2667 of consensus"
repeat_region 34111. .34427
/note="MER31A repeat: matches 4. .477 of consensus"
35235. .35300
/note="MER5A repeat: matches 121. .189 of consensus"
35369. .35435
repeat_region

Query Match 38.0%; Score 332.8; DB 9; Length 132449;
Best Local Similarity 99.4%; Pred. No. 7.7e-77;
Matches 334; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 540 gccgcctcagaatctgaaattcggccttcacgaagaactgtaatgacgaagt 599
|||||
DB 82186 GCCGCTCCGGGAATTCGAAGTCTGGCCCTTCTCGAAGACGTATGATGACCTGAAGT 82245
|||||
QY 600 ttctgaatatcgcaaacccgcaagattagcctgctgctgcacaaagaagaacacat 659
|||||
DB 82246 TTCGGAATATTCGCAAAACCCACAGATTAGCGTGGCTGCCCAAAAGAAACACACAT 82305
|||||
QY 660 agagtttaagatccagtagtgaattgaaactgttttcatttgaagctgaatatata 719
|||||
DB 82306 AGAGTTTAAGATCCAGTAGAGATTGTAACCTGTTTCATTTGAAGCTGAATATATA 82365
|||||
QY 720 cgtatgctatgttatgttggaactaagagatatctttagcaagaagaataatttccc 779
|||||
DB 82366 CGTAGTCATGTTATGTTGGAACACTAAGAGATATCTTTAGCAAGAAATATTTCCCC 82425
|||||
QY 780 ttatcccaactgctgtagagtttcttacctgcttgatgctgtaagatccgaga 839
|||||
DB 82426 TTATCCCACTGCTGTGAGAGTTTCTGTACCTGCTTGAGATCCTGTAAGATCCGGGA 82485
|||||
QY 840 gccctgcgcaactgctgtgtgctgctgcgc 875
|||||
DB 82486 GCCTTGCCGACATGCTTGTGGTGCGCTGCGCTC 82521
|||||

RESULT 9
AC044842 AC044842 172307 bp DNA HTG 25-JUN-2000
LOCUS Homo sapiens chromosome 2 clone RP11-178E20 map 2, WORKING DRAFT
DEFINITION SEQUENCE, 23 unordered pieces.
ACCESSION AC044842
VERSION AC044842.2 GI:8705156
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Birren,B., Linton,L., Nusbaum,C. and Lander,E.
AUTHORS 1 (bases 1 to 172307)
TITLE Homo sapiens chromosome 2, clone RP11-178E20
```



```

misc_feature /note="assembly_fragment"
67980..78235
misc_feature /note="assembly_fragment"
7836..89176
misc_feature /note="assembly_fragment"
89277..106081
misc_feature /note="assembly_fragment"
106182..121387
misc_feature /note="assembly_fragment"
121488..137207
misc_feature /note="assembly_fragment"
137308..153745
misc_feature /note="assembly_fragment"
153846..172307
BASE COUNT 44249 a 40378 c 41592 g 43880 t 2208 others
ORIGIN

```

```

Query Match 37.9% Score 331.2; DB 2; Length 172307;
Best Local Similarity 99.1% Pred. No. 2e-76;
Matches 333; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 540 gccgcctcagaatctgaaattcttgcccttctcagaagacgtgaatgtaactgaagt 599
|||||
DB 114132 GCCGCTCCAGAAATTAAGAAATTTGGGCTTTCTCAGAAACATGTAATGACCTGAAGT 114191
|||||
QY 600 ttctgaatatctgaaacccagagattagctgctgctcgaagaagaagaagaat 659
|||||
DB 114192 TTTTGAATAATTGCAAAACCCACAGATTAGGCTGCTGCTCCANAAAGAAAGCAACAT 114251
|||||
QY 660 agagtttaagatcagtagagattgtaaacctgttttcaatttgaagctgaatata 719
|||||
DB 114252 AGAGTTTAAGATTCAGTAGAGATTGTAACCTGTTTCATTTGAAGCTGAATATATA 114311
|||||
QY 720 cgtagtcagtctgtagaactgaagatactcttagaagaagaagaatatttcccc 779
|||||
DB 114312 CGTAGTCAGTGTGTTGTTGGAACAACTAATGATTTTTCAGCAAGAAATAATTTTCCCC 114371
|||||
QY 780 ttatccccacgtgctgtagagttctgtaacctgctgtagagctgtagaagatcccgaga 839
|||||
DB 114372 TTATCCCACTGCTGTGAGGTTCTGTGACCTGCTGTGATGCTGTGAAGATCCCGAGA 114431
|||||
QY 840 gccctgcgcacgtcctgtgtgctgctgcgc 875
|||||
DB 114432 GCCTTGCCGCACTGCTGTGTGCTGTGCGCTTC 114467

```

```

RESULT 10
LOCUS AK000383 2196 bp mRNA PRI 22-FEB-2000
DEFINITION Homo sapiens cDNA FLJ20376 fls, clone HUV01087.
ACCESSION AK000383
VERSION AK000383.1 GI:7020436
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens primary endothelial cells of human umbilical vein cDNA
to mRNA, clone_lib:HUV clone:HUV01087.

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
Taniigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K.,
Hirao,M., Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished (2000)
2 (bases 1 to 2196)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo, Department
of Virology, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan

```

(E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).

```

FEATURES
source
1..2196
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="primary endothelial cells of human umbilical
vein"
/clone="HUV01087"
/clone_lib="HUV"
/note="Cloning vector pME18SFL3"
BASE COUNT 520 a 540 c 599 g 537 t
ORIGIN

```

```

Query Match 36.0% Score 315.4; DB 9; Length 2196;
Best Local Similarity 99.7% Pred. No. 2.7e-72;
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 224 aagacattcagaagaatattatattcattcagagtgccgctccgctgtagagctg 283
|||||
DB 1 AAGACATTTCGAAGAAATATTAAATTCATTCAGCAGTCCGCGCTCCGCGGTGAAGCTG 60
|||||
QY 284 cctgtacacgtcctgcgcgggtctcagagagctgtaacactgtgatcgcatacat 343
|||||
DB 61 CCTGTACACGCTCCGCGCGGCTCCAGCAGCTGACACGTGATCGCATATCATAT 120
|||||
QY 344 gaccgtcaactctgtgctgtagagagtgcccttgacaccgctgctgcggtagactctg 403
|||||
DB 121 GACCTTCACGACTTTGCTGTGGAGATGCCCTGCACACCGCTGCTGTGGAGATCCTG 180
|||||
QY 404 tgcacaccccaacgtggtcttcacagagacgtcagagattgtagaagcatgaagtcga 463
|||||
DB 181 TGCCAAACCCCAAGTGGGCTTCAGAGACAGCTCCAGAGATTGGAAGCATGAGCTCA 240
|||||
QY 464 tcaagatcgcagctgctgtagaagaatattgtagagagagcccttgcagatgcagaaga 523
|||||
DB 241 TCAGTATCGGCGAGCTGCTGGAAGCAATATGAGAGAGACCCCTTTCAGAGATGACAGA 300
|||||
QY 524 agcccaaaaacattctgg 540
|||||
DB 301 AGCCAAAAACAATTCGG 317

```

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RESULT 11
LOCUS AX068347 687 bp DNA PAT 25-JAN-2001
DEFINITION Sequence 20 from Patent WO0102582.
ACCESSION AX068347
VERSION AX068347.1 GI:12578516
KEYWORDS
SOURCE house mouse.
MUS musculus

```

```

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 687)
Luciw,R.M. and Wel,B.
Dsp-3 dual-specificity phosphatase
Patent: WO 0102582-A 20 11-JAN-2001;
Ceptlyr, Inc. (US)
TITLE Location/Qualifiers
JOURNAL

```

```

FEATURES
source
1..687
/organism="Mus musculus"
/db_xref="taxon:10090"
BASE COUNT 181 a 169 c 197 g 140 t
ORIGIN

```

[illegible]

OY 413 caacgttgagctccagagacagctccagagattgagaaagatgaggtccacag 467
|||||
Db 167120 CAACCTGGGCTTTCAAGGACGCTGCAGAGCTTTGAGAAACATGAGTGCACGAG 167174

RESULT 13
G19642/c

LOCUS G19642 260 bp DNA STS 24-JUL-1996
DEFINITION human STS A001745, sequence tagged site.

ACCESSION G19642

VERSION G19642.1 GI:1340213

KEYWORDS STS: STS sequence; primer; sequence tagged site.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 260)

AUTHORS Adams, M.D.

JOURNAL Unpublished (1996)

COMMENT

Contact: Mark Adams

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Email: mdadams@igf.org

Primer A: ACACAAACGAGAGAAAC

Primer B: GATATCCTTTAGCAAGAGAA

STS size: 260

PCR Profile:

Denaturation: 96C 5min

Anneal: 54C 30sec

Extend: 72C 30sec

Denature: 95C 30sec

FinalExtend: 72C 5min

Cycles: 30

Protocol:

GenomicDNA: 25 ng

Primer: 0.43 uM each

dNTPs: 230 uM each

Amplifrag: 0.5 units

TagStart Ab: 0.5 units

Total Volume: 10 uL

Buffer:

Trits-HCl pH8.8: 100 mM

KCl: 500 mM

MgCl2: 20 mM

Triton X-100: 1%

Concentration: 10X

Prepared with primer pairs derived from THC9390; GenBank Accession

Numbers-- D20266, T30540.

Location/Qualifiers

SOURCE

1..260

/db_xref="taxon:9606"

STS

primer_bind

complement(241..260)

BASE COUNT

81 a 71 c 66 g 41 t 1 others

ORIGIN

Query Match

14.4%; Score 126.4; DB 11; Length 260;

Best Local Similarity 99.2%; Pred. No. 1.6e-22;

Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 748 gatattcttgaagaagaaatatttcccttaccactgctgagagatttcgt 807

|||||

Db 260 GATATCCTTTAGCAAGAGAAATATTTCCCTTAATCCCACTGCTGAGAGTTCTGT 201

|||||

OY 808 acctgcttgatgctctaaagatccggagagcttgcgacgtgctgtggtgct 867

|||||

Db 200 ACCTGCTTGATGCTCTTAAGATCCGGAGGCTTGGCCGACTGCTTGAGGTGCT 141

OY 868 tggcgctc 875

|||||

Db 140 TGGCGCTC 133

RESULT 14
AX180881

LOCUS AX180881 1326 bp DNA PAT 06-AUG-2001

DEFINITION Sequence 8 from Patent WO0146394.

ACCESSION AX180881

VERSION AX180881.1 GI:15132709

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1326)

AUTHORS Plowman, G.D., Martinez, R., Whyte, D., Manning, G., Sudarsanam, S.,

Hill, R.J., and Flanagan, P.

Mammalian protein phosphatases

Patent: WO 0146394-A 8 28-JUN-2001;

JOURNAL Sugen, Inc. (US)

FEATURES

Location/Qualifiers

1..1326

/db_xref="taxon:9606"

BASE COUNT 239 a 437 c 410 g 240 t

ORIGIN

Query Match 13.8%; Score 120.4; DB 6; Length 1326;

Best Local Similarity 56.1%; Pred. No. 6.2e-21;

Matches 303; Conservative 0; Mismatches 166; Indels 51; Gaps 2;

OY 35 tgcgcctgagaccacagcgccgagcgctagcgttcgcttcagccacatgaggatgg 94

|||||

Db 234 TTCCGGGCGGGGAGAGCTGGGGGTGCACCGGACCGCGCGGGGAGATGCGCAATGG 293

OY 95 gatgaacaagatcctgcccgcctgtacatggcaacttcaagaatgccaagagcgagg 154

|||||

Db 294 CATGACCAAGGATCTTCCTGACCTCCTGGAACCTTGAATGACCAAGACCTGGA 353

OY 155 acaattgagcaagaacagatgacacatatctgtctgccaaga-tagtcgaagcctat 213

|||||

Db 354 TCAGCTGGGCGCAAAATTAAGATACACACATCATCTCTATCATGAGTCAACCCAGCTCT 413

OY 214 gttagagacaagacat----- 230

|||||

Db 414 GCTGACGATATACCTTACCTGCAATCCGCTGATACCCGTGAGGTACCATCA 473

OY 231 -----ttcaagaagaatattaaatcaatcaagagtgccgctccggtgagagctg 283

|||||

Db 474 AAGACATTTCAAGATGATATCACTTCACTGCTGCGCTTAATGAGGGGGAATCG 533

OY 284 ccttgtaactgctcgtgcccgggtgtccagagagtgtaacgtgtagatgcatatcat 343

|||||

Db 534 CTTTGTGACATCTTGTGACAGGATCTCTGACACACAGATTTGACAGCGCTATGTGAT 593

OY 344 gaccgtgaactgtgctgagagatgacctgcaacacgctgctgcccggagagatcctg 403

|||||

Db 594 GACTGTGACGGGGCTTAGGCTGGGAGCTGCTTAAGCATCAAGCCATCAAGGCGCT 653

OY 404 tgcacaaccacagctgagcttccagagacagctccagagagttgagaagcatgagtgca 463

|||||

Db 654 CCGCAACCCCAACAGGCTTTAGCAGACGCTTGAAGAGTTGGCTGGGCGAGTTCCA 713

OY 464 ttagatagggcgtgctgtaaggaagaatagtagagagagaccccttgcagagatgcagaaga 523

|||||

Db 714 GAAGCTTCCCGGACGCTGAGGAGCGCTTGGCGAGAGCCCTTCGCGAGAGAGGA 773

```

RESULT 15
AL133540 87616 bp DNA HTG 10-JUL-2001
LOCUS AL133540/c
DEFINITION Homo sapiens chromosome 6 clone RP1-125A24 map p24.1-25.3, ***
ACCESSION AL133540
VERSION AL133540.8 GI:9884658
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 87616)
REFERENCE
AUTHORS Burton, J.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Aug 22, 2000 this sequence version replaced gi:9863453.
COMMENT
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: dj125A24
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 81220 bases at least Q40
Consensus quality: 83782 bases at least Q30
Consensus quality: 85419 bases at least Q20
Insert size: 86816; sum-of-contigs
Insert size: 106856; 2.2% error; agarose-fp
Quality coverage: 2.96x in Q20 bases; sum-of-contigs Quality
coverage: 2.54x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
3452: contig of 3452 bp in length
3453 3552: gap of 100 bp
3553 23206: contig of 19654 bp in length
23207 23306: gap of 100 bp
23307 33410: contig of 10104 bp in length
33411 33510: gap of 100 bp
33511 35989: contig of 2479 bp in length
35990 36089: gap of 100 bp
36090 51429: contig of 15340 bp in length
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51530 56298: contig of 4769 bp in length
56299 56398: gap of 100 bp
56399 62780: contig of 6382 bp in length
62781 62880: gap of 100 bp
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/chromosome="6"
/map="p24.1-25.3"
/clone="RP1-125A24"
/clone_id="RPT-1"
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/misc_feature
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vector_side:left"
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23307..33410
/note="assembly_fragment:00236.0"
33511..35989
/note="assembly_fragment:00554"
36090..51429
/note="assembly_fragment:00398"
51530..56298
/note="assembly_fragment:00410"
56399..62780
/note="assembly_fragment:00571"
62881..66439
/note="assembly_fragment:00783"
66540..87616
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vector_side:right"
BASE COUNT 25196 a 18263 c 19295 g 24060 t 802 others
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Query Match 12.0% Score 105.2; DB 2; Length 87616;
Best Local Similarity 93.2%; Pred No. 6.7e-17;
Matches 110; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 cccgcgcgtccctcctcctgaacatgcatagtcgctgcgacacacgcccgggc 60
DB 33277 cccgcgcgtccctcctcctgaacatgcatagtcgctgcgacacacgcccgggc 33218
QY 61 gctagcgttcgcttcacgaccacatgaggatgagatgaacagatcctgcgcgcct 118
DB 33217 gctagcgttcgcttcacgaccacatgaggatgagatgaacagatcctgcgcct 33160

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Search completed: February 13, 2002, 02:10:38
Job time: 5251 sec

Thu Feb 14 16:00:22 2002

us-09-544-525-1.rge

Page 13

DR P-PSDB; AAB23298.

XX Novel dual-specificity mitogen activated protein kinase phosphatase
PT polypeptide useful in screening assays for identifying agents that
PT modulate activity of the protein which are useful for treating cancer
PS and autoimmune diseases

Claim 7; Fig 1; 60pp; English.

CC The invention relates to a human dual-specificity mitogen-activated
CC protein (MAP) kinase phosphatase, DSP-3, and to nucleic acids encoding
CC it. The invention also relates to variants of DSP-3 which retain
CC activity, expression vectors and host cells comprising DSP-3-encoding
CC DNA, the recombinant production of DSP-3, an anti-DSP-3 antibody, and
CC a DSP-3 substrate-trapping mutant protein that has a reduced ability to
CC dephosphorylate a substrate relative to the wild-type DSP-3. The
CC invention additionally encompasses use of a DSP-3 modulator to modulate
CC a proliferative response, cell differentiation or cell survival. The
CC DSP-3 protein is useful for screening an agent that binds to DSP-3 and/or
CC modulates DSP-3 activity, and is also useful for raising antibodies. DNA
CC encoding DSP-3 or a reporter protein is also useful for screening an
CC agent that modulates DSP-3 activity. The identified agents that
CC modulate DSP-3 activity are useful for treating Duchenne muscular
CC dystrophy, cancer, graft-versus-host disease, autoimmune diseases,
CC allergies, metabolic diseases, abnormal cell growth, abnormal cell
CC proliferation and cell cycle abnormalities. DSP-3-specific antibodies
CC and DSP-3 antisense probes are useful for detecting DSP-3 expression in
CC a sample. The present sequence represents cDNA encoding human DSP-3.

XX Sequence 875 BP; 218 A; 217 C; 231 G; 209 T; 0 other;

Query Match 99.8%; Score 873.4; DB 21; Length 875;
Best Local Similarity 99.9%; Pred. No. 4.8e-255;

Matches 874; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 61 gctagcgttcgcttcacgcacacatggtggaatggaagaagaatcctgcgcgcctgt 120
DB 61 gctagcgttcgcttcacgcacacatggtggaatggaagaagaatcctgcgcgcctgt 120
OY 61 gctagcgttcgcttcacgcacacatggtggaatggaagaagaatcctgcgcgcctgt 120
DB 61 gctagcgttcgcttcacgcacacatggtggaatggaagaagaatcctgcgcgcctgt 120
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DB 301 ccgggggtccagagagcgtgacatcgtgatcgcatatataatgacccctcgtgcttg 360
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DB 361 gctggagagatgcccctgcacacgcgtgcgtccgagagatacctgttccaaacccaacgtgg 420
OY 421 gcttcacagacagctccagagatttggagaacatgagatccatcatcgtgcagctggc 480
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DB 541 cccgtccaggaattctgagcttcctgcgccttctccagaagactgtaaatgtaacctgaagt 600
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DB 601 tctgaataatctgcaaaccccgacagatttagctgtgtcgtccaaaagaagaacacata 660
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DB 661 gagtttaagatccagtagtattgttaactgttttcatcttgaagctgaatatatc 720
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DB 721 gtagtcaatcttatcttggagaactaaggaatcttcttaagaagaagaataatctccct 780
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DB 781 tatccccaactgtgtgagagttctctgtacactgcgttgatgctgctgtaagatcccgagg 840
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DB 841 ccttgcgcacactgccttgggtggtgctggcgtc 875

RESULT 2
ID AAF32191
AAAF32191 standard; cDNA; 926 BP.
XX AAF32191;
AC AAF32191;
XX 12-APR-2001 (first entry)
DE Human dual-specificity phosphatase DSP-3 coding sequence.
XX Human; DSP-3; dual-specificity phosphatase; cell proliferation;
KW cell signalling; cancer; graft-versus-host disease; autoimmune disease;
KW allergy; metabolic disease; Duchenne muscular dystrophy; ss.
OS Homo sapiens.

XX WO200102581-A1.
PN 11-JAN-2001.
PD 20-APR-2000; 2000WO-US10868.
PE 02-JUL-1999; 99US-0142338.
PR 07-APR-2000; 2000WO-US09185.
XX (CEPT-) CEPTYR INC.
PA Luche RM, Wei B;
PI WPI; 2001-138148/14.
DR P-PSDB; AAB67167.
XX New dual-specificity phosphatase-3 polypeptide and its variants useful
PT for treating disorders associated with DSP-3 activity, defects in cell
PT proliferation, differentiation or survival, e.g. Duchenne muscular
PT dystrophy, cancer

PS Claim 7; Fig 1; 70pp; English.

CC The present invention provides the protein and coding sequences of the
CC human dual-specificity phosphatase DSP-3. The DSP-3 protein is involved
CC in cell signalling and the sequences can be used in the treatment of
CC cancer, metabolic and autoimmune diseases, allergies, graft-versus-host
CC disease, abnormal cell proliferation and Duchenne muscular dystrophy.

XX Sequence 926 BP; 233 A; 230 C; 242 G; 221 T; 0 other;

Query Match 91.7%; Score 802.4; DB 22; Length 926;


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DB 241 tcccaagcagcgaattccacatccaactgaacagacattccaagaagatataat 300
QY 250 tcaattacagagtgccgcgtccgcggtgagagcgtgcttgtaacctgctggccggggtct 309
DB 301 tcaattacagagtgccgcgtccgcggtgagagcgtgcttgtaacctgctggccggggtct 360
QY 310 ccagagcgtgacacgtgcatcgatcacatcatgacccgtcactgcttgctgctggag 369
DB 361 ccagagcgtgacacgtgcatcgatcacatcatgacccgtcactgcttgctgctggag 420
QY 370 atgacctgcaacccgtgctgctggagagatcctgccaaccccaacgtgggtctcaga 429
DB 421 atgacctgcaacccgtgctgctggagagatcctgccaaccccaacgtgggtctcaga 480
QY 430 gacagctcaaggagtttgagaagcagcagtgatcatcagatcagcagctgctgtaagaag 489
DB 481 gacagctcaaggagtttgagaagcagcagtgatcatcagatcagcagctgctgtaagaag 540
QY 490 aataatgagagagcccttgcaagatgcagaagaagccaaaacattctggccgcctcag 549
DB 541 aataatgagagagcccttgcaagatgcagaagaagccaaaacattctggccgcctcag 600
QY 550 gaattctgaagctcggcccttctcagaagacgtgaatgtaacctgaaagttctgaata 609
DB 601 gaattctgaagctcggcccttctcagaagacgtgaatgtaacctgaaagttctgaata 660
QY 610 ttgcaaacccgcagagtttaggtggtgctgccaataaagaagaacacatagagtttaag 669
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DB 721 tatccagtagtgattgtaacctgttttcaatttgaagctgaataatacagtaagtcag 780
QY 730 ttatgttgagaactaagaatattcttgaagaagaataatttcccttatcccccac 789
DB 781 ttatgttgagaactaagaatattcttgaagaagaataatttcccttatcccccac 840
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DB 901 actgccttggtggtgctggcgcctc 926

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RESULT 4
AAF63568
ID AAF63568 standard; cDNA; 1379 BP.
XX AAF63568;
DT 11-MAY-2001 (first entry)
DE Human phosphatase AA374753.h coding sequence.
XX
XX Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia;
KW cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia;
KW congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease;
KW Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;
KW schizophrenia; hamartoma; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200112819-A2.
PN
XX
XX 22-FEB-2001.
PD
XX
XX 11-AUG-2000; 2000WO-US22158.
PF

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XX PR 13-AUG-1999; 99US-0149005.
XX PA (SUGEN-) SUGEN INC.
XX PI Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;
XX DR WPI: 2001-211226/21.
XX DR P-PSDB: AAB73216.
XX PT New protein phosphatase polypeptide for diagnosing and treating
XX PT phosphatase related disorders such as cancer, schizophrenia, cardiac
XX PT dysfunction and/or vascular disorders
XX PS Claim 1; Fig 4; 138pp; English.
XX CC The present invention relates to phosphatase proteins and coding
XX CC sequences. The present sequence is one such phosphatase coding sequence.
XX CC Phosphatases are enzymes that catalyse the dephosphorylation of proteins
XX CC modified by phosphorylation of serine, threonine or tyrosine residues.
XX CC The phosphatases are useful for treating a variety of diseases: for
XX CC example cancer e.g. breast, urogenital, prostate, head, neck, lung
XX CC cancers, synovial sarcomas, renal cell carcinoma, non-small cell lung
XX CC cancer, hepatocellular carcinoma, pancreatic endocrine tumours, stomach
XX CC cancer, glioblastoma, colorectal cancer and thyroid cancer,
XX CC pathophysiological hypoxia, cardiac dysfunction and/or vascular
XX CC disorders, myopathies, congenital muscle disorders, Papillon-Lefevre
XX CC syndrome, Cowden disease, ectodermal dysplasia, Moebius syndrome,
XX CC Bjornstad syndrome, Bannayan Zonana syndrome, schizophrenia and
XX CC hamartomas.
XX SQ Sequence 1379 BP; 298 A; 374 C; 386 G; 320 T; 1 other;

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Query Match 91.3%; Score 799.2; DB 22; Length 1379;
Best Local Similarity 94.2%; Pred. No. 2,1e-232;
Matches 872; Conservative 0; Mismatches 3; Indels 51; Gaps 2;

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DB 317 gctagcgttcgcttcaagcaccatgaggaatggaatgaagaagatcctgcccgcct 376
QY 121 acatcgcaactccaagaatgacagagacgcggaacaattggaagaagaagaagtgcac 180
DB 377 acatcgcaactccaagaatgacagagacgcggaacaattggaagaagaagaagtgcac 436
QY 181 atattcgtctgtccagatagt-ccagggcctatgttgag----- 220
DB 437 atattcgtctgtccagatagtgtccagggcctatgttgagggagttaatcctgtgca 496
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DB 497 tcccaagcagcgaattccacatccaactgcagaagaacattccaagaagatataat 556
QY 250 tcaattacagagtgccgcgtccgcggtgagagcgtgcttgtaacctgctggccggggtct 309
DB 557 tcaattacagagtgccgcgtccgcggtgagagcgtgcttgtaacctgctggccggggtct 616
QY 310 ccagagcgtgacacgtgcatcgatcacatcatgacccgtcactgcttgctgctggag 369
DB 617 ccagagcgtgacacgtgcatcgatcacatcatgacccgtcactgcttgctgctggag 676
QY 370 atgacctgcaacccgtgctgctggagagatcctgccaaccccaacgtgggtctcaga 429
DB 677 atgacctgcaacccgtgctgctggagagatcctgccaaccccaacgtgggtctcaga 736
QY 430 gacagctcaaggagtttgagaagcagcagtgatcatcagatcagcagctgctgtaagaag 489
DB 737 gacagctcaaggagtttgagaagcagcagtgatcatcagatcagcagctgctgtaagaag 796

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YY	490	aataatgagagagaccccttgcagagatgcagagaagccaaaaacattctgcgcgtccag	549
YY	491		
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QY	550	gaattctgaagttcttgcgcttcttcagaagactglaatgtaccgtgaagttcttgaata	609
Db	857	gaattctgaagttcttgcgcttcttcagaagactglaatgtaccgtgaagttcttgaata	916
QY	610	ttgcaaacccgcagagtttagctgtgtctgtccaaagaagaagcaacatagagtttag	669
Db	917	ttgcaaacccgcagagtttagctgtgtgtgtccaaagaagaagcaacatagagtttag	976
QY	670	tatccagtaagtattgtataactgttttcaatttgaagctgtaataatactagtaatg	729
Db	977	tatccagtaagtattgtataactgttttcaatttgaagctgtaataatactagtaatg	1036
QY	730	tttatgtttgagaactaagatatattctttagaagaagaataattttcccttatccacc	789
Db	1037	tttatgtttgagaactaagatatattctttagaagaagaataattttcccttatccacc	1096
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QY	850	actgcctgtgtggtgtgcttgcgcctc	875
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AC	AAZ46164:		
XX	16-MAY-2000	(first entry)	
DE	cDNA sequence encoding a human phosphorylation effector PHSP-27.		
XX			
KW	Human; phosphorylation effector; PHSP; proliferative disorder;		
KM	immune disorder; neuronal disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
EH	Key	Location/Qualifiers	
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PN	W0200006728-A2.		
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PD	10-FEB-2000.		
XX			
PF	28-JUL-1999;	99NO-US17132.	
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PR	28-JUL-1998;	98US-0123494.	
PR	14-SEP-1998;	98US-0152814.	
PR	14-OCT-1998;	98US-0173482.	
PR	03-NOV-1998;	98US-0106889.	
PR	19-NOV-1998;	98US-0109093.	
PR	22-DEC-1998;	98US-0113796.	
PR	12-JAN-1999;	98US-0173482.	
PR	12-JAN-1999;	99US-0229005.	
XX			
PA	(INCYT-) INCYTE PHARM INC.		
PI	Hillman JL, Lai P, Tang YT, Corley NC, Guegler KJ, Baughn MR;		
PI	Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y,		
XX	Reddy R, Lu DM, Shih LL;		
XX	WPI: 2000-183125/16.		
DR	P-PSDB; AAY68795.		

Pt	New human phosphorylation effectors useful for the diagnosis, treatment
xx	and prevention of proliferative, immune and neuronal disorders -
xx	
ps	Claim 9; Page 139; 142pp; English.
xx	
cc	AZA6138-746168 encode human phosphorylation effectors (PSP),
cc	designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given
cc	in the specification). The sequences were isolated from cDNA libraries
cc	prepared from various human tissues. The PSP proteins are useful for
cc	the diagnosis, treatment and prevention of proliferative disorders,
cc	immune disorders and neuronal disorders. The PSP proteins form
cc	pharmaceutical compositions which useful for treating or preventing
cc	disorders associated with decreased PSP expression/activity. PSP
cc	antagonists are useful for treating or preventing disorders associated
cc	with increased PSP expression/activity.
xx	
SQ	Sequence 1290 BP; 299 A; 341 C; 339 G; 311 T; 0 other;
	Query Match 91.2%; Score 797.6; DB 21; Length 1290;
	Best Local Similarity 94.1%; Pred. No. 6.3e-232;
	Matches 871; Conservative 0; Mismatches 4; Indels 51; Gaps 2;
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QY	61 gctagcgttcgcttcaagcacaccatggggaaatgggatgacaagaattcctgccgcgt 120
Db	
	215 gctagcgttcgcttcaagcacaccatggggaaatgggatgacaagaattcctgccgcgt 274
QY	121 acatcgcgaacttcaaagaatgtccagagacgcygaacaalttgacagaacaagtgtcac 180
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	275 acatcgcgaacttcaaagaatgtccagagacgcygaacaalttgacagaacaagtgtcac 334
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QY	310 ccagagacgtgacaactgtgtgatcgcatatcataatgaacogtcaactgtgtgtggag 369
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	515 ccagagacgtgacaactgtgtgatcgcatatcataatgaacogtcaactgtgtgtggag 574
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RESULT 6
AAf86152
ID      AAF86152 standard; cDNA; 1218 BP.
XX
AC      AAF86152;
XX
DT      29-JUN-2001 (first entry)
XX
DE      Human JNK activating phosphatase (JNKAP) cDNA.
XX
KW      C-Jun amino-terminal kinase; JNK; JNK activating phosphatase; JNKAP;
KW      dual-specificity phosphatase; ischemic heart disease; kidney failure;
KW      cardiac hypertrophy; burn; liver damage; respiratory distress syndrome;
KW      septic shock; rheumatoid arthritis; autoimmune disorder; human;
KW      inflammatory disease; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
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FT      /note= "JNK activating phosphatase"
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PD      29-MAR-2001.
XX
PF      21-SEP-2000; 2000WO-US25948.
XX
PR      21-SEP-1999; 99US-0155068.
XX      20-SEP-2000; 2000US-0665819.
XX
PA      (AMGE-) AMGEN INC.
PA      (BAYV) BAYER COLLEGE MEDICINE.
XX
PI      Tan T, Zhou G, Belmont JW, Fletcher FA, Chen AJ, Jurecic R;
XX
FI      WPI: 2001-316103/33.
XX      P-PSDB: AAB81105.
XX
PT      New human or mouse C-Jun amino-terminal kinase (JNK) activating
PT      phosphatase is useful for diagnosing or treating diseases associated
PT      with JNK activating phosphatase or JNK-mediated disorders, e.g.
PT      inflammatory diseases
XX
PS      Claim 1; Fig 1; 116pp; English.
XX
CC      This invention relates to human or murine C-Jun amino-terminal kinase
CC      (JNK) activating phosphatase (JNKAP). The present sequence represents
CC      human cDNA encoding JNKAP. The JNKAP protein has an amino-terminal
CC      dual-specificity phosphatase domain and lacks a non-catalytic
CC      carboxy-terminal domain. The protein has functional activities comprising
CC      dual-specificity phosphatase activity and JNK pathway upregulation
CC      activity. The JNKAP polypeptide can be used for diagnosing a JNK-mediated
CC      disorder or a susceptibility to a JNK-mediated disorder, and for
CC      identifying a compound which binds to it. The JNKAP polypeptide and

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CC      nucleic acid molecules are useful in screening for therapeutic agents to
CC      treat, prevent and/or detect conditions relating to JNK mediated
CC      disorders, e.g. ischemic heart disease, cardiac hypertrophy, burns due
CC      to heat or radiation, kidney failure, liver damage due to oxidative
CC      stress or alcohol, respiratory distress syndrome, septic shock,
CC      rheumatoid arthritis, autoimmune disorders, or other types of
CC      inflammatory diseases. The polypeptides may also be used for screening
CC      therapeutic agents for treating a disease involving cytokine production
CC      in an animal, and for identifying agents that modulate the JNK signal
CC      transduction pathways. The nucleic acid molecules encoding JNKAP are
CC      useful for mapping the locations of the JNK activating phosphatase gene
CC      and related genes on chromosomes; as anti-sense inhibitors of JNK
CC      activating phosphatase polypeptide expression; or for gene therapy.
XX
SQ      Sequence 1218 BP; 251 A; 340 C; 363 G; 264 T; 0 other;

Query Match      53.2%; Score 465.8; DB 22; Length 1218;
Best Local Similarity 91.0%; Pred. No. 3.7e-131;
Matches 538; Conservative 0; Mismatches 2; Indels 51; Gaps 2;

Qy      1  cccgcgcgtctctctctctctctgtaacatgcatagtcgccttgccagcacacgcccgggc 60
Db      98  cccgcgcgtctctctctctctctctgtaacatgcatagtcgccttgccagcacacgcccgggc 157
Qy      61  gctagcgttcgcttccagccaccatgagggaatggatgaacaagatcctgcgcgcgtgt 120
Db      158  gctagcgttcgcttccagccaccatgagggaatggatgaacaagatcctgcgcgcgtgt 217
Qy      121  acatcgcaacttcaaaagatgcccagagacgcggacaattgacgaagaacagtggaac 180
Db      218  acatcgcaacttcaaaagatgcccagagacgcggacaattgacgaagaacagtggaac 277
Qy      181  atattctgtctgtccacgaatgt-ccaggcctatgtgag----- 220
Db      278  atattctgtctgtccatgatagtgccagcgccatgttgaggaggttaatacctgtgca 337
Qy      221  -----gacaagacattcaagaagtataat 249
Db      338  tcccgacgagcgaattaccacatctcaaaccttgacacatttcaagaagtataat 397
Qy      250  tcattcacgagtgcgcgtccgcggttgagagctgctgtatacactgcctgcgcgggtct 309
Db      398  tcattcacgagtgcgcgtccgcggttgagagctgctgtatacactgcctgcgcgggtct 457
Qy      310  ccaagagcgttgacactgtgtatcgcatatcatatgaccgttaactgtactgttcggag 369
Db      458  ccaagagcgttgacactgtgtatcgcatatcatatgaccgttaactgtactgttcggag 517
Qy      370  atgcctctgacacacggtgcgtgcgggagatcctgtgcaaccaccaagtggttccaga 429
Db      518  atgcctctgacacacggtgcgtgcgggagatcctgtgcaaccaccaagtggttccaga 577
Qy      430  gacagctccagagattgagaagcatgaggtccatcaatccgacagatggttgaagaag 489
Db      578  gacagctccagagattgagaagcatgaggtccatcaatccgacagatggttgaagaag 637
Qy      490  aatatgagagagcccttgcaggatgcaagaagaccnaaaactctg 540
Db      638  aatatgagagagcccttgcaggatgcaagaagaccnaaaactctg 688

RESULT 7
AAf63565
ID      AAF63565 standard; cDNA; 1067 BP.
XX
AC      AAF63565;
XX
DT      11-MAY-2001 (first entry)
XX
DE      Murine phosphatase AA103595_m coding sequence.
XX
KW      Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia;

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KM	cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia;
KM	congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease;
KM	Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;
KM	schizophrenia; hamartoma; ss.
OS	Mus sp.
XX	
PN	WO200112819-A2.
XX	
PD	22-FEB-2001.
XX	
PF	11-AUG-2000; 2000WO-US221158.
XX	
PR	13-AUG-1999; 99US-0149005.
XX	
PA	(SUGEN-) SUGEN INC.
XX	
PI	Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;
DR	WPI: 2001-211226/21.
XX	P-PSDB: AAB73213.
PT	
PT	New protein phosphatase polypeptide for diagnosing and treating
XX	phosphatase related disorders such as cancer, schizophrenia, cardiac
XX	dysfunction and/or vascular disorders
PS	Claim 1; Fig 4; 136pp; English.
XX	
CC	The present invention relates to phosphatase proteins and coding
CC	sequences. The present sequence is one such phosphatase coding sequence.
CC	Phosphatases are enzymes that catalyse the dephosphorylation of proteins
CC	modified by phosphorylation of serine, threonine or tyrosine residues.
CC	The phosphatases are useful for treating a variety of diseases: for
CC	example cancer e.g. breast, urogenital, prostate, head, neck, lung
CC	cancers, synovial sarcomas, renal cell carcinoma, non-small cell lung
CC	cancer, hepatocellular carcinoma, pancreatic endocrine tumours, stomach
CC	cancer, glioblastoma, colorectal cancer and thyroid cancer,
CC	pathophysiological hypoxia, cardiac dysfunction and/or vascular
CC	disorders, myopathies, congenital muscle disorders, Papillon-Lefevre
CC	syndrome, Cowden disease, ectodermal dysplasia, Moebius syndrome,
CC	Bjornstad syndrome, Bannayan Zonana syndrome, schizophrenia and
CC	hamartomas.
XX	
SO	Sequence 1067 BP; 287 A; 229 C; 266 G; 285 T; 0 other:
Query Match	51.5%; Score 450.8; DB 22; Length 1067;
Best Local Similarity	78.7%; Pred. No. 1,2e-126;
Matches 645; Conservative	0; Mismatches 102; Indels 73; Gaps 6
QY	51 cggccggcgagcgtacgttcgccttcacgaccacatgsgggagatgacaagaatcctg 110
DB	
QY	9 cggcgagcgcgagcgagcgcgccgcgcgcgcacatggggatgagccagatcctg 68
QY	111 cccggcctgtacatcgcgcaactcaagaatgccagagacgcggacaattgsgcaagaac 170
DB	
QY	69 ccggcgctcatcattgtgcaacttcaagaagcgaagaagatgacagaacagttgsgcagaac 128
QY	171 aaggtgaacatatctctgtgtccagatagt-ccaggccatattgtgag----- 220
DB	
QY	129 aaggtgaacacatctcttctgttgcaagatactgccaagcccatgttgagggagttaa 188
QY	221 -----gacagacattcaaga 239
DB	
QY	189 tacctgttattccagcgcgacacacacatctcaaaactgtacaagaacatttcaaga 248
QY	240 agtataaattcaatcacagatgtccggctccgcggtgagagctgttcctgttacctgct 299
DB	
QY	249 agcataaattcatcatgagtgccgacatccaggtgagagctgttctgttacctgtcctg 308
QY	300 gccggggtctccagagaggtgacactgtgtgacatcagataatcatgacgcgtacctactt 359
DB	
QY	309 gctggggtctccagagaggtgacactgtgtgacatcagataatcatgacctaccgcactt 368

[illegible]

QY 327 gtagcgcacatcatcagcactgactgcttgctggagagatgacctgacacgctg 386
 |||||
 Db 322 gtgacgcacacacacacagactgctacacgacttgctggagagatgacctgacacgctt 381
 QY 387 cgtgcccggagatcctgtgccaaccccaacgctggctccagacagacgctccagagctt 446
 |||||
 Db 382 cgtgcccggagatcctgtgccaaccccaacgctggctccagacagacgctccagagctt 441
 QY 447 gagaagacatgagtcacatcagatcggcagtgctgaagagaataatgagagagccct 506
 |||||
 Db 442 gagaacacatgagtcacacgctgacatgctgagagagaagatgagagagacccct 501
 QY 507 ttgcagagatgcagaagaagcaaaacattctgg 540
 |||||
 Db 502 ttgcgagatgcagaagaagcaaaacattctgg 535
 RESULT 10
 AAF86153
 ID AAF86153 standard; cDNA; 3010 BP.
 AC AAF86153;
 XX 29-JUN-2001 (first entry)
 DE Murine JNK activating phosphatase (JNAP) cDNA.
 XX C-Jun amino-terminal kinase; JNK; JNK activating phosphatase; JNAP;
 KW dual-specificity phosphatase; ischemic heart disease; kidney failure;
 KW cardiac hypertrophy; burn; liver damage; respiratory distress syndrome;
 KW septic shock; rheumatoid arthritis; autoimmune disorder; mouse;
 KW inflammatory disease; chromosome 13; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT 15..632
 FT CDS /*tag= a
 FT /product= "JNAP"
 FT /note= "JNK activating phosphatase"
 XX
 PN W0200121812-A1.
 XX 29-MAR-2001.
 PD
 PF 21-SEP-2000; 2000WO-US25948.
 XX
 PR 21-SEP-1999; 99US-0155068.
 PR 20-SEP-2000; 2000US-0665819.
 XX
 PA (AMGE-) AMGEN INC.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Tan T, Zhou G, Belmont JW, Fletcher FA, Chen AJ, Juretic R;
 DR WPI; 2001-316103/33.
 DR P-PSDB: AAB81106.
 XX
 PT New human or mouse c-Jun amino-terminal kinase (JNK) activating
 PT phosphatase is useful for diagnosing or treating diseases associated
 PT with JNK activating phosphatase or JNK-mediated disorders, e.g.
 PT inflammatory diseases
 XX
 PS Claim 1; Fig 2; 116pp; English.
 CC This invention relates to human or murine c-Jun amino-terminal kinase
 CC (JNAP) activating phosphatase (JNAP). The present sequence represents
 CC murine cDNA encoding JNAP. The murine JNAP gene has been mapped to
 CC chromosome 13. The JNAP protein has an amino-terminal dual-specificity
 CC phosphatase domain and lacks a non-catalytic carboxy-terminal domain. The
 CC protein has functional activities comprising dual-specificity phosphatase
 CC activity and JNK pathway upregulation activity. The JNAP polypeptide can

CC be used for diagnosing a JNK-mediated disorder or a susceptibility to a
 CC JNK-mediated disorder, and for identifying a compound which binds to it.
 CC The JNAP polypeptide and nucleic acid molecules are useful in screening
 CC for therapeutic agents to treat, prevent and/or detect conditions
 CC relating to JNK-mediated disorders, e.g. ischemic heart disease, cardiac
 CC hypertrophy, burns due to heat or radiation, kidney failure, liver damage
 CC due to oxidative stress or alcohol, respiratory distress syndrome, septic
 CC shock, rheumatoid arthritis, autoimmune disorders, or other types of
 CC inflammatory diseases. The polypeptides may also be used for screening
 CC therapeutic agents for treating a disease involving cytokine production
 CC in an animal, and for identifying agents that modulate the JNK signal
 CC transduction pathways. The nucleic acid molecules encoding JNAP are
 CC useful for mapping the locations of the JNK activating phosphatase gene
 CC and related genes on chromosomes, as anti-sense inhibitors of JNK
 CC activating phosphatase polypeptide expression, or for gene therapy.
 XX
 SQ Sequence 3010 BP; 746 A; 702 C; 742 G; 819 T; 1 other;
 Query Match 35.0%; Score 306.2; DB 22; Length 3010;
 Best Local Similarity 79.1%; Pred. No. 1.9e-82;
 Matches 412; Conservative 0; Mismatches 58; Indels 51; Gaps 2;
 QY 71 gcttcagccacccatggtggatggtatgaacagatcctgcccggcctgtatcgcgca 130
 |||
 Db 2 gcccgccgagcagatggtggatggtatgacagatcctgcccggcctgtatcgcgca 61
 QY 131 ctccaagaatgcccagagacgagcagcaatltgaagcaagaaggtgacacatctctc 190
 |||||
 Db 62 ctccaagaatgcccagagacgagcagcaatltgaagcaagaaggtgacacatctctc 121
 QY 191 tgcacacatggt-ccaagcctatgttgaag----- 220
 |||||
 Db 122 tgtgcagatattcgcagagcccatggttggaggttaatacctgtattccagcgc 181
 QY 221 -----gacaagacattccaagaagatlaaattcaatcaca 259
 |||||
 Db 182 agacacacatctcaaaacccgacagacattccaagaagatlaaattcaatcaca 241
 QY 260 gtgcgcgctccgagtgagagctgctgtacactgctgcccggggtctcagaagcgt 319
 |||||
 Db 242 gtgcgcgctccgagtgagagctgctgtacactgctgcccggggtctcagaagcgt 301
 QY 320 gacactgtgtgcacatcatcagcactgactgcttgctggagagtgccctca 379
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 Db 302 gacactgtgtgcacatcatcagcactgactgcttgctggagagtgccctca 361
 QY 380 caccgtgctgcggagatcctgtgccaaccccaacgctggctccagacacgctca 439
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 Db 362 caccgtgctgcggagatcctgtgccaaccccaacgctggctccagacacgctca 421
 QY 440 ggaagttgagaagaatgagtcacatcagatcggcagtgctgaagagaataatgaga 499
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 Db 422 ggaagttgagaagaatgagtcacatcagatcggcagtgctgaagagaataatgaga 481
 QY 500 gaagccttgcagagatgcagaagaagcccaaaacattctgg 540
 |||||
 Db 482 gaagccttgcagagatgcagaagaagcccaaaacattctgg 522
 RESULT 11
 AAC75779
 ID AAC75779 standard; cDNA; 289 BP.
 AC AAC75779;
 XX
 DT 08-FEB-2001 (first entry)
 DE Human OREFX ORF134 polynucleotide sequence SEQ ID NO:2667.
 DE Human; open reading frame; OREFX; detection; cytostatic; hepatotropic;
 KW antiviral; antiparkinsonian; antiparkinsonian; neurotrophic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;

immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 hypotensive; dermatological; immunosuppressive; antineoplastic;
 antiviral; antibacterial; antifungal; antineuritic; antihypertensive;
 antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 neurodegenerative disorder; osteoarthritis; graft vs host disease;
 cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 cholesterol ester storage; systemic lupus erythematosus; infection;
 severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 bone damage; cartilage damage; antineoplastic disease; coagulation;
 thrombosis; contraceptive; ss.
 Homo sapiens.
 WO200058473-A2.
 05-OCT-2000.
 31-MAR-2000; 2000WO-US08621.
 31-MAR-1999; 99US-0127607.
 02-APR-1999; 99US-0127636.
 05-APR-1999; 99US-0127728.
 30-MAR-2000; 2000US-0540763.
 (CURA-) CURAGEN CORP.
 Shinkens RA, Leach M;
 WPI: 2000-602362/57.
 P-PSDB; AAB41570.
 Novel nucleic acids and peptides derived from open reading frame X,
 useful for treating e.g. cancers, proliferative disorders,
 neurodegenerative disorders and cardiovascular disease -
 Claim 5; Page 1910-1911; 5507pp; English.
 AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB4397,
 which represent the human ORF open reading frames 1 to 3161. The ORF
 sequences have activities such as: cytosolic; hepatotropic; vulnary;
 antiproliferative; antiparkinsonian; nocrotropic; neuroprotective;
 osteoprotective; anticonvulsant; antiallergic; immunosuppressant;
 immunostimulant; cardiact; thrombolytic; coagulant; vasotropic;
 antidiabetic; hypotensive; dermatological; immunosuppressive;
 antineoplastic; antibacterial; antiviral; antifungal; antineuritic;
 antihypertensive; antianemic. The sequences can be used for determining
 the presence of or predisposition to, or preventing or treating
 pathological conditions associated with an ORF-associated disorder. The
 nucleic acids can be used to express ORF proteins in gene therapy
 vectors. The proteins and nucleic acids may be used to treat cancers,
 proliferative disorders, neurodegenerative disorders, osteoarthritis,
 graft vs host disease, cardiovascular disease, diabetes mellitus,
 hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 nocturnal haemoglobinuria, antineoplastic disease, to enhance
 coagulation; to inhibit thrombosis; and as a contraceptive.
 Sequence 289 BP; 71 A; 71 C; 84 G; 62 T; 1 other;
 Query Match 28 3%; Score 247.6; DB 21; Length 289;
 Best Local Similarity 95.8%; Fred. No. 3e-65;
 Matches 276; Conservative 0; Mismatches 9; Indels 3; Gaps 2;
 QY 82 ccatgggaatggatgacaaagatccgcccgcctgtacatggcgaattcaagatg 141
 Db 2 ccatgggaatggatgacaaagatccgcccgcctgtacatggcgaattcaagatg 61
 QY 142 ccagagacgaggaacatgtgacaaagatg-acacatattctgtccacat 200

Db 62 ccagagacgaggaacatgtgacaaagatgacaaagatccctttctgttcccgat 121
 QY 201 ag- tccagcctatgttggagacaaagatcttcaaaagatataatcatcag 258
 Pb 122 ggggtccagcctatgttggagacaaagatcttcaaaagatataatcatcag 181
 QY 259 agtgcgagtcgcggttggagatcgtctgtacacgtgacggtgcctccagagcg 318
 Db 182 agtgcgagtcgcggttggagatcgtctgtacacgtgacggtgcctccagagcg 241
 QY 319 tgacactgtgacatcacatcacatgacgcgtactgacttggctggg 366
 Db 242 tgacactgtgacatcacatcacatgacgcgtactgacttggctggg 289
 RESULT 12
 AAD09498
 ID AAD09498 standard; DNA; 1326 BP.
 AC AAD09498;
 XX 10-SEP-2001 (first entry)
 XX Human SGP008 phosphatase polypeptide encoding DNA.
 DE Human SGP008 phosphatase polypeptide encoding DNA.
 XX Human: SGP008 phosphatase polypeptide: phosphatase-related disease;
 KW immune-related disorder; ocular disease; organ transplant rejection;
 KW infection; diabetes; pain; sexual dysfunction; Alzheimer's disease;
 KW metabolic disorder; haematopoietic cancer; mood disorder; cardiact;
 KW parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis;
 KW cardiovascular disease; brain; neuronal-associated disease; dyskinesia;
 KW attention disorder; cognition disorder; psychotic disorder; cytosolic;
 KW neurological disorder; virinicide; nocrotropic; cerebroprotective; therapy;
 KW neuroprotective; antibacterial; vulnary; tranquilliser; antistimulant;
 KW hypotensive; immunosuppressive; antiproliferative; analgesic; hypertensive;
 KW antifungal; dual specificity phosphatase; DSP; MAP kinase phosphatase;
 KW MKP; migraine; chromosome 20q11.2; ds.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..971
 FT CDS
 FT /*tag= a
 FT /product= "Human SGP008 phosphatase polypeptide"
 FT /transl_except= (pos:967..971, aa:LSKGGK)
 FT /note= "CDS does not include stop codon"
 FT /partial
 XX WO200146394-A2.
 Pn 28-JUN-2001.
 XX 21-DEC-2000; 2000WO-US34736.
 XX 21-DEC-1999; 99US-0173255.
 XX 28-DEC-1999; 99US-0175766.
 PR 25-JAN-2000; 2000US-0178078.
 PR 31-JAN-2000; 2000US-0179301.
 XX (SUGEN-) SUGEN INC.
 PA Plowman GP, Martinez R, Whyte D, Manning G, Sudarsanam S, Hill RJ;
 PI Flanagan P;
 XX WPI: 2001-418058/44.
 DR P-PSDB; AAE04840.
 XX Novel phosphatase polypeptide useful for treating cancers,
 PT immune-related diseases and disorders, cardiovascular disease, brain or
 PT neuronal-associated diseases and metabolic disorders -
 XX Claim 29; Fig 1; 186pp; English.

CC Kinase phosphatase (MKP). SGP003 gene maps to chromosomal position
CC CHR10.

XX
SQ Sequence 1262 BP; 287 A; 356 C; 392 G; 227 T; 0 other;

Query Match 6.7%; Score 58.6; DB 22; Length 1262;
Best Local Similarity 57.6%; Pred. No. 1.8e-07;
Matches 125; Conservative 0; Mismatches 89; Indels 3; Gaps 1;

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QY 284 cctgtacactgctggccggggtctccagagagctgacactggtgatacatcat 343
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Db 668 cctgttcaactgctcatatgggcccagccggtcagccacctgtgctctactgat 727

QY 344 gaccgtactgacttggcttggagagatgccctgcacacgctgcgtgccgggagatcctg 403
    || | | | | | | | | | | | | | | | | | | | | | | | | |
Db 728 gatcacagaagacatgacccctggtgagcgcacatccagcaagtg--gccaaagaaccgctg 784

QY 404 tgcacaaccacaagctgggcttccagagacagctccagagagtttgagaagcatgagtcga 463
    | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 785 cgtctctccggaaccggtgttlttgaaagcagctccgggagctggacaagcagctgtgca 844

QY 464 tcagtatcggaagtggctggaaggaagatatggagag 500
    ||| || | | | | | | | | | | | | | | | | | | | |
Db 845 gcagagggcagcgtcccaagccaggaagcgtgaggaag 881
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Search completed: February 13, 2002, 02:11:26
Job time: 313 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2002, 00:37:13 ; Search time 1214.51 Seconds

(without alignments)
7741.852 Million cell updates/sec

Title: US-09-544-525-1

Perfect score: 875
Sequence: 1 cccgcgcgcctcctccct.....ttgtggtgcttgacgcctc 875

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estlin:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hlc:*
10: gb_est1:*
11: gb_est2:*
12: gb_hlc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588.6	67.3	717	10	AV714942
2	559	63.9	915	11	BE868556
3	538.8	61.6	819	11	BE910217
4	530.2	60.6	665	11	BE532390
5	520.6	59.5	694	10	AV764304
6	499.6	57.1	589	10	AW963729
7	458.6	52.4	950	11	BE674814
8	445.8	50.9	751	11	BE545679
9	442.2	50.5	447	10	AA410486
10	389.8	44.5	502	10	AV711945
11	365	41.7	554	10	BE292273
12	357.4	40.8	371	10	AA374753

13	336.4	38.4	354	10	AA411633
14	326.4	37.3	464	10	AA256096
15	323.4	37.0	945	13	A0743659
16	309	35.3	569	11	B1158161
17	308.8	35.3	366	10	AA625487
18	307.4	35.1	411	11	N36626
19	305.4	34.9	510	10	AM188661
20	303.6	34.7	465	10	AM385663
21	301.6	34.5	496	11	BE549803
22	296.4	33.9	495	10	AA406582
23	295.4	33.8	493	10	AA847680
24	280.4	32.0	481	10	AM167272
25	278.4	31.8	478	10	AM151243
26	273.4	31.2	474	10	AM621715
27	272.4	31.1	412	10	AV764531
28	271.6	31.0	502	11	N25994
29	270.2	30.9	734	11	BE697122
30	270	30.9	589	11	BE854383
31	260.4	29.8	262	10	AA284022
32	257.6	29.4	415	10	AA827049
33	254	29.0	458	10	AM513605
34	253.4	29.0	454	10	AI829183
35	252	28.8	448	10	AI290229
36	249.6	28.5	458	10	AM413206
37	242.4	27.7	1020	11	BE862745
38	241.2	27.6	463	10	AA815315
39	241	27.5	459	11	R70442
40	233.6	26.7	491	10	BE753729
41	232	26.5	429	10	AI818989
42	231	26.4	475	11	B1360910
43	230.8	26.4	439	10	AI040507
44	230.2	26.3	417	11	H42445
45	230	26.3	648	10	AI171617

ALIGNMENTS

RESULT 1
LOCUS AV714942 717 bp mRNA EST 11-OCT-2000
DEFINITION AV714942 DCB Homo sapiens cDNA clone DCBBJ09 5', mRNA sequence.
ACCESSION AV714942
VERSION AV714942.1 GI:10796459
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 717)
Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)

TITLE
JOURNAL
COMMENT
Contact: Zengang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Shanghai
201203, P. R. China
Tel.: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..717
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DCBBJ09"
/clone_lib="DCB"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"

BASE COUNT 205 a 160 c 182 g 170 t /note="Vector: pTriplet2; Site_1: sfilA; Site_2: sfilB"
 ORIGIN

Query Match 67.3%; Score 588.6; DB 10; Length 717;
 Best Local Similarity 92.3%; Pred. No. 6.3e-156;
 Matches 662; Conservative 0; Mismatches 4; Indels 51; Gaps 2;

OY 100 acaagatctgcccgcgcgtacatgaggaactcaagaatgccagaagcgggaacat 159
 |||||||
 Db 1 ACAGATCTCTGCCCGGCTTACATGGCACTTCAAGATGCCAAGACGCGGAACAT 60
 OY 160 tgaagcaagaacagtgacacatatctgtctgccaagatg-ccaagccatgttg 218
 |||||||
 Db 61 TGAGCAAGAACAAGTGACACATATCTGCTGTCCACGATATGCGAGCCCATATGTTG 120
 OY 219 ag-----gacaagac 228
 ||
 Db 121 AGGAGATTAAATACCTGTGATCCAGACGCGATTCAACATCTCAAAACCTGCAAGAC 180
 OY 229 attcaagaagaagtataatcaatcagagtgccggtccggtgagagctgcttg 288
 |||||||
 Db 181 ATTTCAAAGAAATATTAAATTCATCAGAGTCCGCGCTCGGCTGAGAGCTGCTTG 240
 OY 289 taactgtccctggccggggtctccagaagcgtgacactgtgtgacatcatcatgaccg 348
 |||||||
 Db 241 TACACTGCTGGCGGGGCTCCAGAGAGGTGACACTGATGCAATCATCATATACCG 300
 OY 349 taactgacttggctgggagagatgcccgcacacgctgctgcccggagatccctgtgca 408
 |||||||
 Db 301 TCAGTGACTTTGGCTGGGAGATGCCCTGCACACCTGCTGCGGAGATCCTGTGCCA 360
 OY 409 accccaagctgggcttcacagacagctccagaagtttgaagaagcagtgagctccatc 468
 |||||||
 Db 361 ACCCCACAGTGGCTTCCAGAGACAGCTCCAGAGATTGAAGAGCATGAGTCCATCACT 420
 OY 469 atcggcagtgctggaagaagataatgagagagagcccttgcagaatgagaagaagcca 528
 |||||||
 Db 421 ATCGGAGTGGCTGAAGAGAAATATGAGAGAGGCCCTTTCAGAGATGCAAGAAAGCCA 480
 OY 529 aaaaacatctggccgctccagaatctcgaagttcctggccttccagaagactgta 588
 |||||||
 Db 481 AAAACATTTCTGGCCGCTCCAGGAATTTCAAGTTTGGGCTTTCAGAAACATGTAT 540
 OY 589 gfacctgaagttctgaatatgtgaacccgcagaagtttaagctggtgctcccaaaag 648
 |||||||
 Db 541 GTACCTGAAGTTTCTGAATATTTGCAAAACCCACAGAGTTTAAAGTGTGCTCCCAAAAG 600
 OY 649 aaaaagaacatagatttaagatcagatgagattggaactgttttcatctgaag 708
 |||||||
 Db 601 AAAAGCAACATAGAGTTTAAGATTCACAGTAGATTTGAAAACCTGTTTATTATTGAAG 660
 OY 709 ctgaatatatacgtatgcatgtttatgttgaagaactaagatatctttaagaagag 765
 |||||||
 Db 661 CTGAATATATACGTAGTATGTTTATGTGAGAACTAAAGATATCTTATAGCAAGAG 717

RESULT 2
 LOCUS BE868556 915 bp mRNA EST 20-OCT-2000
 DEFINITION 601444589P1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848374 5',
 mRNA sequence.
 ACCESSION BE868556
 VERSION BE868556
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 915)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9564 row: b column: 23
 High quality sequence stop: 693.
 Location/Qualifiers

FEATURES

source 1..915
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3848374"
 /clone_1ib="NIH_MGC_65"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."
 BASE COUNT 248 a 221 c 242 g 204 t
 ORIGIN

Query Match 63.9%; Score 559; DB 11; Length 915;
 Best Local Similarity 86.3%; Pred. No. 1.6e-147;
 Matches 698; Conservative 0; Mismatches 55; Indels 56; Gaps 5;

OY 86 ggggaatgagatgaacaaatctctgcccgcgtgtacatcgtgcaacttcaagaagcag 145
 |||||||
 Db 8 GGGGAATGGGATGAACAAATATCTCGCCGCTGTACATCGGCAACTCAAGATCCAG 67
 OY 146 agaagcgaacaatttgaagaagaagtgacatatctgtctgtccacagatg-c 204
 |||||||
 Db 68 AGACGGGAAACATTTAGCAACAAGGTGACATATTTCTGTCTCCAGATATGTC 127
 OY 205 caggccatgttgag----- 220
 |||||||
 Db 128 CAGGCTTATGTTGGAGGAGATTAAATACCTGTGATCCCATCAGCGGATTCACATCTCA 187
 OY 221 -----gacaagacatttcaagaagatataatcattcaaggtgcggctccggg 274
 |||||||
 Db 188 AAACCTGACAAAGACATTTCAAGAAAGTAATTAATTCATTCACGATGCGGCTCCGGG 247
 OY 275 tgaagctgacctgtgacactgctgcccgggtctccagaagcgtgacactgtgactgc 334
 |||||||
 Db 248 TGAGAGCTGCTTGTACACTGCTTGCCGGGCTTCCAGAGACGCTGACACTGCTGATCGC 307
 OY 335 atacatcatgacgtcactgacttggctgggagagatgccctgcacacgctgctgcgg 394
 |||||||
 Db 308 ATACATCATAGACGCTACACTGACTTGGCTGGGAGATGCCCTGCACACGCTGGCTGCG 367
 OY 395 ggaatcctgtgccaaccccaacgtgtgcttccagaagacgtccagaagtttgaaga 454
 |||||||
 Db 368 GAGATCTGTGCCAACCCCAACGTTGGCTTCCAGAGACAGCTCCAGGAGTTTGAAGACA 427
 OY 455 tgaagtcacatgactgagcagtggtcgaagaagaatatggaagagcccttgcaga 514
 |||||||
 Db 428 TGAGTCCATCATCTATCGGCACTGCTTAAGAGAAATATGAGAGAGCCCTTGCACAGA 487
 OY 515 tgcagaagaagccaacaaatcttgcgcgtccagaagattcgaagtttgcgcttct 574
 |||||||
 Db 488 TGCAAGAAAGCAAAAACATTTCTGCGCTCCGGAATTCGAAGTTCTGGGCTTTCT 547
 OY 575 cagaagactgtatgtactcgtgaagtttctgaataatgcaaacccgcagaagtttagctg 634
 |||||||
 Db 548 CAGAAGACTGTAAATGTACTGAAAGTTTCTGAATATGCAAGACACAGAGTTTAAAGCTG 607
 OY 635 gtgcgtccaaaaagaagaacacatagagtttaagttacccagttgltgtaactgt 694

Db 608 GTGCTGCCAAAAGAAAGACATAGAG-TTAACTATCCAGTGTATTTGTAACCTG 666
 QY 695 ttcttcattgaagcttaataataataacagtagatgattatgtgagaactaagatattc 754
 Db 667 GATTTCATTGAGCTG-ATATATAGAGTACATGATGTCACGTGAGAACTCAGATATTC 725
 QY 755 tttagcaagaagaataatttcccttatcccaactgctgtgaggtttctgtacccgc 814
 Db 726 TTAAGC--AGAGAAACATTTCCTTAATCCCATGCTGTGCAAGCTTACAGCTTCG 782
 QY 815 ttgagtcctgttaagatcccgagagcct 843
 Db 783 TTGAGAGGCTGTAAAGATCCGGAACCTT 811

RESULT 3
 BE910217 819 bp mRNA EST 20-OCT-2000
 LOCUS BE910217 601503530F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905407 5',
 DEFINITION mRNA sequence.
 ACCESSION BE910217
 KEYWORDS BE910217.1 GI:10406586
 SOURCE EST.
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 819)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: L1AM9712 row: k column: 08
 High quality sequence stop: 731.
 Location/Qualifiers
 1. 819
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:3905407"
 /clone_id="NIH_MGC_70"
 /tissue_type="epithelioid carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pCMV-SPOK6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.1 kb. Library constructed by Life
 Technologies."

BASE COUNT 216 a 178 c 218 g 207 t
 ORIGIN

Query Match 61.6%; Score 538.8; DB 11; Length 819;
 Best Local Similarity 99.3%; Pred. No. 8.5e-142;
 Matches 562; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 311 caggagcgtgacactggt-gatcgatatacatcatgacgtcactgacttggctggagag 369
 Db 1 CAGGAGCGTGAACACTGTGTGATCGCATACATACACCGTACCTTGGCTGGAGG 60
 QY 370 atgcccctgacacgcgtgctgctggagatctctgtgccaaaccccaagctggctccaga 429
 Db 61 ATGCCCTGCACACCGCTGCTGTGGAGATCTGTGCCAACCCCAACGCTGGCTTCACA 120
 QY 430 gacagctcagaggtttagaagcatgagtcacatcatgagcagtgagctgaagagag 489
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 121 GACAGCTCCAGAGTTTGAGAAGCATGAGTCCATCACTATTCGGAGTGCTGAAGAG 180
 QY 490 aatatgagagagagcccttgcagagatgcagagaagaagccaaaacatttgcgcctcag 549
 Db 181 AATATGAGAGAGGCCCTTTGAGAGATGCAAGAAAGCCAAATTCCTGGCCCTCAG 240
 QY 550 gaattcgaagtctggagccttctcagaagaactgtaatgacacgaatttcgaata 609
 Db 241 GAATTCGTAAGTTCTGGGCCCTTTTCAGAAACATGTAATGTAACGAAATTCGAATA 300
 QY 610 ttgcaaacccgcaagatttaagctgctgtccaaaagaagaagaacatagagttlaag 669
 Db 301 TTGCAAAACCCACAGAGTTTAGGCTGCTGCCAAAAAGAAAGCAATAGAGTTTAA 360
 QY 670 taccagtagtattgttaactgttttcaatttgaagctgaatatatacagtagcatg 729
 Db 361 TATCAGTAGATGATTTGTAACCTGTTTTCATTGTAAGCTGTAATATACGTAAGTAT 420
 QY 730 ttatgttgagaactaagatatctttagcaagaagaataatttcccttatcccaac 789
 Db 421 TTTATGTTGAGAACATMAAGATATCTTTAGCAAGAAATATTTCCCTTATCCCAAC 480
 QY 790 tgcgtgagagtttctgtaactgcttgatgagcctgttaagatcccgagagccttgccg 849
 Db 481 TGCCTGGAGGTTTCTGTACTCGCTTGATGCTGTAAAGATCCCGAGCCTTGCCG- 539
 QY 850 actgctgtggtgctgctgagcctc 875
 Db 540 ACTGCTGTGAGGTTGCTGCTTGAGCTGCTGAGATCCCGAGCCTTGCCG- 565
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RESULT 4
 BG532390 665 bp mRNA EST 03-APR-2001
 LOCUS BG532390 602561902F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4699705 5',
 DEFINITION mRNA sequence.
 ACCESSION BG532390
 VERSION BG532390.1 GI:13523928
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 665)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONETECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: L1CM1532 row: c column: 02
 High quality sequence stop: 663.
 Location/Qualifiers
 1. 665
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:4699705"
 /clone_id="NIH_MGC_61"
 /tissue_type="embryonal carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcgccctggcc); Site_2: SfiI (ggcgctttagc).
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCCATTAATGAGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGGCGGCGGCGAGCATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average

[illegible][illegible]

REFERENCE	Hegde, P., Qi, R., Abernethy, K., Dhara, S., Gaspar, R., Gay, C., Holtz, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeaman, T.J. and Quackenbush, J.
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	unpublished (2000)
COMMENT	Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 3528
Fax: 301 838 0208
Email: johnget@igr.org
Plate: 192
Seq primer: Reverse.

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FEATURES
source      Location/Qualifiers
1..589      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE ressequences, MAGE"
/note="vector: pBluescriptSM"
BASE COUNT  157 a      138 c      162 g      132 t
ORIGIN
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Query Match	57.1%	Score 499.6	DB 10	Length 589
Best Local Similarity	95.4%	Pred. No. 1e-130		
Matches 536	Conservative	0	Mismatches 24	Indels 2
			Gaps	2

QY	93	ggagatgaacaaagatccctgcccgcgccttaactcgcgaacttcaagaatgcacagaacgc	152
Db	1	GGCACTAGCAAGATCTCTCCCGGGCTGTGCATAGGCAATTCAAAGATGCCACAGACGG	60
QY	153	gaacaattgagcaagaacaagtgltacacatactctgctgtccacgaatag - coagcct	211
Db	61	GAACATTTGACCAAGAACAAAGTACACATTTCTGTCTGTCCACGATTAATGCCAGGCT	120
QY	212	atgltggagagacaagaacattccaagaagaatataatcaattcaagatgcccgcctcg	271
Db	121	ATGTTGGAGGACAAAGACATTTCAAGAAGATTAATTAATTCATTCACGATGCCGCTCCG	180
QY	272	cggatgagagctgacctgttaacatcgcctgcccgcggtctccaagagacgltgaactgtgat	331
Db	181	CGGTGAGAGCTGCGCTTGATACACTCCCTCGCGCGGCTGCCAGGAGCGCTGACACTGAT	240
QY	332	cgcatacaactaagccgtaactgacttggctgtggaagatgaccttgaaacccgtgtgc	391
Db	241	CGCATACATCATGACCGGTCACTTGCTGTGGAGAGATGCCCTGCACACCGTGCCTGC	300
QY	392	cggagagatccgtgtccaaccccacaacgtggagcttccagaagacagctccaagaattggaa	451
Db	301	TGGGAGATCTGTGTCACACCCCAACGTGGGCTTCCAAAGACAGCTCCAGAGATTGGAA	360

QY	452	gcacgaagtcacatcagatctcgccagctggccgaagaagaatcagaaagagccctttgca	511
QY	361	gcattgaggtccatcattagatctggcagctggctgaagaaagaattatggaaagagccctttgca	420
Db	512	ggaatgcgaagaagaagcccaaaaacatctctgcgcgtcccaagaatctgaagttctggagcctt	571
QY	421	ggatgcagaaagaaagcccaaaaacattctggccgctccagaaattctgaaagttctggagcctt	480
Db	572	tctcagaagaatctgtaaatgctacccgaaagttctctgaaatatctgcaaaccccgaaagttt-ag	630
QY	481	tctcagaagaatctgtaaatgctacccgaaagtttttgaaataattgcaaaaccccgaaagtttaag	540
Db	631	gctgagtcgtcccaaaagaaga 652	
QY	541	gctgagtcgtcccaaaagga 562	
Db			

RESULT	7
BG674814	
LOCUS	950 bp mRNA
DEFINITION	BG674814 60262094YF1 NCI_CGAP_Skn3 Homo sapiens CDNA clone IMAGE:4746442 5'
ACCESSION	BG674814
VERSION	BG674814
KEYWORDS	BG674814.1 GI:13906210
SOURCE	EST.
ORGANISM	human.

ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE: 1 (bases 1 to 950)
AUTHORS: NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE: National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL: Unpublished. (1999)
COMMENT: Contact: Robert Strausberg, Ph.D.

Email: cgapds-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
Genomic Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10594 row: n column: 11
High quality sequence stop: 815.

FEATURES	SOURCE	Location/Qualifiers
1.	.950	
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="IMAGE:4746442"
		/clone_lib="NCI_CGAP_Skn3"
		/lab_host="DH10B (71 phage-resistant)"
		/note="Organ: skin; Vector: pCMV-SPOK16; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dT
		Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT	246 a	225 c 262 g 217 t
ORIGIN		

Query Match	52.48;	Score 458.6;	DB 11;	Length 950;
Best Local Similarity	81.38;	Pred. No. 4.8e-119;		
Matches 742;	Conservative	0;	Mismatches 94;	Indels 77;

[illegible]

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Db 121 ATTGACCAATTAAGTAGTACTATATTACTAGTCTGTGTCACAGATAGATGCCAGTCT 180
Qy 212 atgttga----- 219
Db 181 ATGTTGGAGGGAGTTAAGATACCTGTGCATCCACAGCGATTCACCGATCTCGAANA 240
Qy 220 ---gacacagacattcaaa-gaaagtattaaattcaatcagagatgccgctccgct 275
Db 241 CCTTGCAAGACATTTCACACGAAATATTAAATTATTCACAGATGCCGCTCCCGAT 300
Qy 276 gagaagctgcttgtaactagctgctgctgctgctcagagagcgtgacgtgac- 334
Db 301 GAGAGCTGCTGTGTACACTGCGTGGCGGGGTCTCCAGAGAGGTGACATGATGATCAGC 360
Qy 335 ataatcatgacccgtca-ctgactttgcttggaagagatgctgacacc-gtgcgtgc 392
Db 361 ATACATCAATGACCGTATGATGCTTGGCTGAGAGATCCCTGAAACACAGAGTCTGCT 420
Qy 393 ggaagatcctgtgcaaccccaacgtggtgcttcacagagacgtccagagatttgaag 452
Db 421 GGGAGATCCTGTGTCACAGCCCAACGTGGCTTCCAGAGACAGTTCAGAGATTGAGAG 480
Qy 453 catgaagtcacatcagatcagcagtgctga--aggaagaaatataggaagagcccttgc 510
Db 481 CATGAGGTCCATCAGATGAGCGAGTGTGACCGGAGACGATGAGAGAGAGCCCTTGC 540
Qy 511 a-ggatgcgaagaagaccacaaa-catttgcgcctccaaga-attctgaattcctgg 567
Db 541 ATGGATGACGAAGAAAGCAAAATATCATVGTGCTGGCTCCGGGACATTCGAAGTGTGG 600
Qy 568 ccttctcagaagactgtta-cttaacctgaatttctgaatatatgcaaacccgagat 626
Db 601 CCTGTCTGAGAAAGACTGTACTGTACTTAAGTTTCTGCCATATGCAAGCCACAGAGAT 660
Qy 627 ttagctgtgctgctgcaaaaaaagaagacaatagatttaagtaaccagtagtattgc 686
Db 661 TTAGGCTGTGCTGCGCAAGGTAGAAAGACATAGAGTTAGTATCCAGTATGCGATTGG 720
Qy 687 taaactgttttcaatttgaagctgaatatatacgtatgcatgttatagttgaagactaa 746
Db 721 TTAACATGTTTTCATTTGAACTGATGATATATACGATAGCATGTCATGTCAGAACTAG 780
Qy 747 ggaattcttag-----caagagaaaaatattcccttacccttgcctgtgctgaggtt 803
Db 781 GGATGATGTCGAGGCAAGAGAACATATTTGGCCCTTAATACCCATATGATGAGAGTTA 840
Qy 804 ct-gtaactgcttgatgctgctgtaagaatcccggaagccttgcgcacgtgcttgc 862
Db 841 CTAGTACCTGCTGCTGATGCTGTAGGATCCGGGAGCCTTGGCGCACTGCTTGTGG 900
Qy 863 tggcttgagctc 875
Db 901 TGGATTGGGGCTC 913

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RESULT 8
LOCUS BG545679 751 bp mRNA EST 04-APR-2001
DEFINITION 602572945F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4701034 5',
ACCESSION BG545679
VERSION BG545679.1 GI:13544344
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 751)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
COMMENT Email: cgabs-r@mail.nih.gov

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Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1535 row: j column: 11
High quality sequence stop: 680.
FEATURES
source
1..751
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4701034"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Lung; Vector: pMDR-LIB (Clontech); Site: 1;
SfiI (ggcgccctggcc); Site: 2; SfiI (ggcgatctggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH-MGC library."
BASE COUNT 189 a 203 c 209 g 150 t
ORIGIN
Query Match 50.9%; Score 445.8; DB: 11; Length 751;
Best Local Similarity 90.7%; Pred. No. 1.9e-115;
Matches 529; Conservative 0; Mismatches 2; Indels 52; Gaps 3;
Qy 10 tccctccctgtaacatgacatgctgctgctgacacacagcgccgggctgagctt 69
Db 2 tctctccctgtaacatgacatgctgctgctgacacacagcgccgggctgagctt 61
Qy 70 cgccttcagccacatgagggaatggatgaaacatccttgcgcgctgtacatcgcga 129
Db 62 ccccttcagccacatgagggaatggatgaaacatccttgcgcgctgtacatcgcga 121
Qy 130 acttcaag-atgccaagagcgggaacatgaaacagcaagtgacacatcttg 188
Db 122 ACTTAAAGTATGCCAGAGACCGGGAACATTTGACCAAGACAGGTGACCATATTTCTG 181
Qy 189 tctgtccagatag-ccaagcctatgttgag----- 220
Db 182 TCTGTCCAGATAGTCCAGGCGCTTATGTTGGAGGGAAGTTAAATACCTGTGATCCACGA 241
Qy 221 -----gacaagacattcaagaaglatataatcaatcac 257
Db 242 GCGGATTCACCATCTCAAAACCTGACAAAGACATTTCAAGAAAGTATTAATTCATTCAC 301
Qy 258 gattgctgctccgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 317
Db 302 GAGTCCGCGCTCCGCGGAGAGAGCTGCTTGTACACTGCTGCGCGGGGTCTCCAGAGAC 361
Qy 318 gtgacactggtatcgcacatcagacgctgacatgctgctgctgctgctgctgctgctg 377
Db 362 GTGACACTGCTGATGCGATACATCATGACCTGATGACTTTGGCTGGAGAGATGCCCTG 421
Qy 378 caacacgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 437
Db 422 CACACCGTGTGCTGCGGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
Qy 438 caggagtttggaagcagatgagatgcatatgagatgagatgagatgagatgagatgagat 497
Db 482 CAGGAGTTTGAAGACATGAGGTCCATCATGATGCGCGCTGAGAGGAATATATGGA 541
Qy 498 gagaagccttgcagagatgacagaaagcgaacaaacattcgg 540
Db 542 GAGAGCCCTTTGCAAGATGCAAGAGACCAACAAATTTCTGG 584

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RESULT      9
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LOCUS
DEFINITION  zv23b12.r1 Soares.NhHMPu_S1 Homo sapiens cDNA clone IMAGE:754463
5', mRNA sequence.
ACCESSION   AA410486
VERSION     AA410486.1  GI:2069654
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 447)
            Hillier,L., Allen,M., Bowles,L., Dubuque,T., Gelsel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
            Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie
            ,T., Waterston,R. and Wilson,R.
            Washu-Merck EST Project 1997
TITLE
JOURNAL
COMMENT
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28ml3 rev2 EF from Amersham
High quality sequence stop: 410.
Location/Qualifiers
1..447
/organism="Homo sapiens"
/db_xref="GDB:5977366"
/db_xref="taxon:9606"
/clone="IMAGE:754463"
/clone_1lb="Soares.NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbM, pregnant uterus
NbHPU, and fetal heart NbH19M) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT  126 a      89 c      115 g      117 t
ORIGIN
Query Match      50.5%; Score 442.2; DB 10; Length 447;
Best Local Similarity 99.3%; Pred. NO. 1.8e-114;
Matches 444; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 354 gacttgctggaagaatgcacctgacacctgctgctggagagatctgtgccaacc 413
DB 1 GACTTTGGCTGGAGAGATGCCCTGCACACCGGCTGCTGGAGATCCTGTGCCAACCC 60
OY 414 aacgtggcttcacagagacgtccagagagttgagaagcatgaagtcacatgacg 473
DB 61 AACGTGGCTTCACAGACAGCTCCAGAGATTGAGAAAGCATGAGCTCATCAGATACGG 120
OY 474 cagtgctgaagaagaatagagagagcccttgacagagatgcagaagaagccaaaac 533
DB 121 CAGTGGCTGAAGGAATATGAGAGAGCCCTTTGCAAGATGCGCAAGAGAGCCCAAAAC 180
OY 534 attcggcgcgtccacagagattctgaagtctggcgcttctcagagaactgtaatgtacc 593

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DB 181 ATTCTGGCCCTCCAGGAATTCGAACTTCGGGCTTTTCAGAGAAGCTGTATGTACC 240
OY 594 tgaagtttcgaaatattgcaaacccagagattagctgctgctccaaaagaag 653
DB 241 TGAAGTTTCGAAATATTGCAAAACCCAGAGATTAGCGTCTGCCCAAAAGAAAG 300
OY 654 caacatgagtttaagatccagtagtgattgtaaacctgttccaattggaagctgaa 713
DB 301 CAACATGAGTTTAAGATATCCAGTAGTAGTATTGTAACCTTTTTCATTGGAAGCTGAA 360
OY 714 tatacagtaagcatgttattgttgaagactaagagatattcttagcaagaagaataatt 773
DB 361 TATATAGTACTCATGTTTATGTTGAGAACGAGATATTTCTTAGCAAGAAATATT 420
OY 774 ttcccttaccacacagctgctgagag 800
DB 421 TTCCCTTATCCACATCCTGTCGAGC 447

RESULT      10
AV711945    502 bp    mRNA    EST    09-OCT-2000
LOCUS
DEFINITION  AV711945 DCA Homo sapiens cDNA clone DCABH12 5', mRNA sequence.
ACCESSION   AV711945
VERSION     AV711945.1  GI:10731251
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 502)
            Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
            Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
            Cheng,Z., Xu,S., Gu,M., Yu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
            ,G., Cheng,Z., and Han,Z.
            Homo sapiens cDNA clones
            Unpublished (2000)
            Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
            Location/Qualifiers
            1..502
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="DCABH12"
            /clone_1lb="DCA"
            /cell_type="dendritic cells"
            /dev_stage="mature"
            /lab_host="BM25.8"
            /note="Vector: pT7ripleX2; Site_1: sfiI; Site_2: sfiIb"
BASE COUNT  142 a      116 c      135 g      109 t
ORIGIN
Query Match      44.5%; Score 389.8; DB 10; Length 502;
Best Local Similarity 95.8%; Pred. NO. 1.3e-99;
Matches 411; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
OY 219 aggaacaagacatllcaagaagaatlaaatcattcacgaagtgccggctccgggtgag 278
DB 75 AGGACAAGACATTTCAAGAAAGATTAATTAATTCATTACAGACTGCCGGCTCCGGTAG 134
OY 279 agctgctctgaactgctgctggcggtctccagagagctgtacactgtgtatgcatac 338
DB 135 AGCTTCCTTTGTAACACTGCTGCGCGGGGCTTCACAGAGAGCTGACACTGCTGTCATAC 194
OY 339 atcatgacgcgtacactgacttggctgggagagatgcccctgcacacacgctgcgtccgggaga 398

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|||||
Db 195 ATCATGACCGTCACTGACTTTGGCTGGAGGATGCCCTGACACCGTGGCTGGAGAG 254
QY 399 tctgtgtccaaaccccaagtggtgtccagagacagctccagaggtttgaagaatgag 458
Db 255 TCGTGTGCCAACCCCAAGCTGGGCTTCAGAGACACCTCCAGAGTTTGAAGCATGAG 314
QY 459 gtccacagatctcgcagtggtcgtgaagaagaatgatggaagagcccttgcagagatga 518
Db 315 GTCCATCAGTATGCGCAGTGGCTGGAAGGAATATGAGAGAGCCCTTTCAGAGATGCA 374
QY 519 gaagaagccaaacacatctgtgcccgtccaggaatctgaagttcgtggcccttctcaga 578
Db 375 AAAAAAGCCAAAACATCTGCGCCGCTCCAGGAATCTGAAGTT-TTGGCCTTTTATA 433
QY 579 agactgtatgtacacctgaagttctgaatatgtcaaccgcagaggttagagctgtgc 638
Db 434 AAACGTAAAGACCCCTGAAGGTTCTGAATATTGCAAAACCCAGAGTTAAGCTGTGC 493
QY 639 tgcacaaaa 647
Db 494 TGCACAAA 502
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LOCUS 601086078P1 NC1_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3500299 5',
DEFINITION mRNA sequence.
ACCESSION BE292273
VERSION BE292273.1 GI:9174552
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 554)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE NIH National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
http://image.llnl.gov
Plate: LLM8558 row: k column: 20
High quality sequence stop: 552.
Location/Qualifiers
1..554
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3500299"
/clone_lib="NC1_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 150 a 129 c 158 g 116 t 1 others
ORIGIN
Query Match 41.7%; Score 365; DB 10; Length 554;
Best Local Similarity 88.8%; Pred. No. 1.4e-92;
Matches 406; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

QY 85 tggggaatggaatgaacaagatctcgtcccgcccttaacttgcgaacttcaagaatgcca 144
Db 1 TGGGAGTGGGATGAGACCGCAGATCTGCCGGGCTGTACATTTGCAACCTTCAAGCGCAA 60
QY 145 gagacgcggaacaatlgaaacaagaagtgacacatctctgtctgcacagatgt- 203
Db 61 GAGATCCAAACAGTTGACAGGAACAGAGTGACACACTTCTTCTGTGACAGATACG 120
QY 204 ccaagccctatgttgagaagcaagaacattcaagaagaatltaattcaatcagagtgac 263
Db 121 CCAGGCCCATGTTGGAGCACAAGACATTTCAAGAAGACATTAATTCATCATGAGTGC 180
QY 264 cggctccgagtggaagagcgtcgttgtaactgtcctgtgcggcggttccagagagtgaca 323
Db 181 CGACTCCAGGTGAGAGCTGCTTGTACATTCCTGCTGGGGGTCTCCAGGAGTGTGACA 240
QY 324 cctggtatgcatacatcatgaaccgtcaactgtgctgtgagagatgacctgcacacc 383
Db 241 TTGGTATGCAATACATCATCATGTGCTGACCGACTTTGGCTGGGAAGATGCCCTTGCACACT 300
QY 384 gtgcgtgccggagatctcgtgtgccaaccccaacgltggcctccagagacagctccaggag 443
Db 301 GTTCGTGCGGGAGGTCTCTGTGCAACCCCACTGGCCTTCAAGGAGCAGCTGCAGAG 360
QY 444 ttggaagcagtgagtgcatcagratatggcagtggtcgtgaagaagaatgatgagaagc 503
Db 361 TTGTGAAACATGAGATGACCATCATGCTGCAATGCTGAGAGAGATGAGAGAAC 420
QY 504 ccttgcagagatgcagaagaagccaaacacattctcg 540
Db 421 CCTTGGCGGATGACGAGAAACCAAAATATTCTGG 457

RESULT 12
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LOCUS EST86937 HSC172 cells 1 Homo sapiens cDNA 5' end similar to similar
DEFINITION to tyrosine phosphatase CL100, mRNA sequence.
ACCESSION AA374753
VERSION AA374753.1 GI:2027073
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 371)
AUTHORS Adams M.D., Kerlavage, A.R., Fletschmann, R.D., Fudner, R.A., Bult
C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White
O., Sutton, G., Blake, J.A., Brandon, R.C., Man, W.L., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D., Fitzgerald,
L.M., Fitzhugh, W.M., Fitchman, J.L., Geophagen, N.S., Glodek, A.,
Guelhm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Kelley, J.M.,
Kelley, J.C., Liu, L., L., Marmaro, S.M., Merick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Fellgrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uteback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferlie, A., Fischer, C., Hastings, G.A., He, W.W.,
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hungjun, J., Li, H., Weisner, P.S., Olsen, H., Raymond, L.,
Wei, Y.F., Wong, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
Venter, J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056

Fax: 3018699423
 Email: arkerlaw@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
 Seq primer: M3 Reverse.

FEATURES

source
 1. 371
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 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):1719154"
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 /clone_lib="HSCI72 cells I"
 /cell_type="fibroblast"
 /cell_line="HSCI72 (16PDL)"
 /dev_stage="fetal"
 /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
 ; Site_2: XhoI"
 BASE COUNT 93 a 97 c 102 g 78 t 1 others
 ORIGIN

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 Best Local Similarity 99.5%; Pred. No. 1.9e-90;
 Matches 369; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 101 caagatccgcccgcctgtacatcggaactcaaatgacagagacgcgacaatt 160
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 Db 1 CAGATCCTGCGCCGCTGTACATCGGCAACTCAAGATGCCAGAGACGGCAACAT 60
 QY 161 gagagaagaagtgacatatctgtctgtccacgagat-ccaggcctatgttga 219
 |||||||
 Db 61 GAGCAAGAACAGGTGACACATATCTGTCTGCACAGATAGTCCAGGCGCTAGTGGGA 120
 QY 220 ggaacagacattcaagaagatlaaatcattccagatgcccgcctccgcggtgaga 279
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 Db 121 GGACAAAGCATTTTAAAGAAAGTATTTAAATTTCACAGATGCCGCTCCGCGTGAGA 180
 QY 280 gctgcctgtacactgctggcgggggtctccagagacgttacactgtgtatcgcataca 339
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 Db 181 GCTGCTGTGACACTGCTGCGCGGGGCTCCAGAGAGGTGACACTGCTGATCCATATCA 240
 QY 340 tcatgaccgtcactgactgtgtgtgagagatgcccctgcacacgcgtgtgcggagagat 399
 |||||||
 Db 241 TCATGACCGGTACGTGCTGGCTGGAGATGCCCTGCACACCGTCTGCTGGAGAT 300
 QY 400 cctgtgcaaccccaacgttggtcttcagagagagctccagagatttgagaagatgagg 459
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 DEFINITION 5', mRNA sequence.
 ACCESSION AA411633 GI:2069430
 VERSION AA411633
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 354)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wyllie,
 J., Waterston, R. and Wilson, M.,
 TITLE Washu-Merck EST Project 1997
 JOURNAL Unpublished (1997)

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 333.

FEATURES

source
 1. 354
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone_lib="IMAGE:753326"
 /clone_lib="Soares_NhHMPu_S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: p7773D-Pac
 (Pharmacia) with a modified polylinker; Site_1: Not I;
 Site_2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte-2NBH, pregnant uterus
 NBHPU, and fetal heart NBH119H) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."
 BASE COUNT 107 a 64 c 79 g 104 t
 ORIGIN

Query Match 38.4%; Score 336.4; DB 10; Length 354;
 Best Local Similarity 99.4%; Pred. No. 1.7e-84;
 Matches 348; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 480 ctgagaagaagaatctggagaagacccttctgagagtcagaagaagccaanaacatttt 539
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 Db 6 CTGAAGGAGAGATATGAGAGAGCCCTTGCAGATG-AGAGAGAGCCAAAGCAATTCG 64
 QY 540 gccgtccagaatctcctaagttctgtggccttccagaagaacttaatgtaacctgaagt 599
 |||||||
 Db 65 GCCGCTCCAGGAATTTCTAAGTTCTGGGCTTTTCACAAGACTGTATGTACCTGAAGT 124
 QY 600 ttctgaatatctgcaaacccgcagagtttaggtgtgtgtcgtccaaaagaagaagaacat 659
 |||||||
 Db 125 TTTCGAATATATGCAAAACCCACAGAGTTAGGCTGTGCTGCCAAGAAAGCAACAT 184
 QY 660 agaatcttaagatccagtagatgttgaactgttttcaatttgaagcgtgaatatata 719
 |||||||
 Db 185 AGAGTTTAAAGTATCCAGTAGTGATGATTTGTAACCTTTTTCATTTGGAAGCTGAATATATTA 244
 QY 720 cgtatcatgttctatgttgaagaactaagatatttcttaagaagaagaataattccccc 779
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 Db 245 CGTACTCATGTATTGTTAGTAGAAGACTAAGATATTTTAAAGCAAGAGAAATATTTTCCCC 304
 QY 780 ttatcccaactgtgtgaggtttctgtacactgctgtgagtctgtaag 829
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 Db 305 TTATCCCACTGCTGTGAGGTTTCTGTACCTCGCTGTGAGATCCCTGTAAAG 354
 RESULT 14
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 LOCUS zsz29b10.tl NC1_GCAP_GCB1 Homo sapiens cDNA clone IMAGE:586587 5',
 DEFINITION mRNA sequence.
 ACCESSION AA256096
 VERSION AA256096.1 GI:1891635
 KEYWORDS EST.
 SOURCE human.

Qy 839 acccttgccgacactgaccttgggtgggttgccgctc 875
|||||
Db 411 Agccttgccgacactgaccttgggtgggttgccgctc 375

Search completed: February 13, 2002, 01:44:45
Job time: 4052 sec

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